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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 03:27:38 ; Search time 10041 Seconds  
(without alignments)  
11561.706 Million cell updates/sec

Title: US-10-053-662A-1  
Perfect score: 3989  
Sequence: 1 tgggtccctctattcacag.....ccagataatgtcttatgt 3989

Scoring table: IDENTITY:NUC  
Gapop 10.0 , Gapept 1.0

Searched: 2054640 seqs, 14551402878 residues  
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_da:\*  
2: gb\_hhg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pi:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_or:\*  
21: em\_ov:\*  
22: em\_pat:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_sts:\*  
27: em\_un:\*  
28: em\_vl:\*  
29: em\_hhg\_hum:\*  
30: em\_hhg\_inv:\*  
31: em\_hhg\_other:\*  
32: em\_hhg\_mus:\*  
33: em\_hhg\_pln:\*  
34: em\_hhg\_rod:\*  
35: em\_hhg\_mam:\*  
36: em\_hhg\_vit:\*  
37: em\_hhg\_vit:\*  
38: em\_hhg\_hum:\*  
39: em\_hhg\_mus:\*  
40: em\_hhg\_other:\*  
41: em\_hhg\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2986.2	74.9	5200	6 AX045561	AX045561 Sequence
2	2986.2	74.9	5200	9 HSLAMB2T	162749 Sequence 12
3	2986.2	74.9	5200	6 AX365737	Z15008 H.sapiens m
4	2956.4	74.1	5156	6 AX365737	AX365737 Sequence
5	2956.4	74.1	5156	6 HSNICE	X73902 H.sapiens m
6	2944.2	72.8	3720	6 AX045565	AX045565 Sequence
7	2880.8	72.2	3620	6 AX045567	AX045567 Sequence
8	2879.2	72.2	5020	6 AX045563	AX045563 Sequence
9	2726	68.3	4316	6 162750	162750 Sequence 14
10	2726	68.3	4316	9 HSLAMB2TB	Z15009 H.sapiens m
11	2652.2	66.5	5158	10 MMU33327	U43337 Mus musculus
12	2590	64.9	5159	6 AX045569	AX045569 Sequence
13	2537.4	63.6	5057	6 AX045571	AX045571 Sequence
14	860.2	21.6	1393	10 MUSNICC	L20477 Mus musculus
15	528.2	13.2	3020	5 AF373841	AF373841 Gallus ga
16	517.4	13.0	7642	10 MUSLAM2B	J03484 Mouse lamin
17	515.6	12.9	4948	6 AX045115	AX045115 Sequence
18	515.6	12.9	4948	6 AX045332	AX045332 Sequence
19	515.6	12.9	4948	6 AX463752	AX463752 Sequence
20	515.6	12.9	4972	6 AX045119	AX045119 Sequence
21	515.6	12.9	5306	6 AX045113	AX045113 Sequence
22	515.6	12.9	5306	6 AX045330	AX045330 Sequence
23	515.6	12.9	5306	6 AX463750	AX463750 Sequence
24	515.6	12.9	5306	6 HUMLAMBB	J03202 Human lamin
25	515.6	12.9	5330	6 AX045117	AX045117 Sequence
26	515.6	12.9	7923	6 AX440444	AX440444 Sequence
27	514.6	12.9	7263	6 AX045123	AX045123 Sequence
28	514.6	12.9	7263	6 AX045336	AX045336 Sequence
29	514.6	12.9	7263	6 AX463756	AX463756 Sequence
30	514.6	12.9	7554	6 AX045121	AX045121 Sequence
31	514.6	12.9	7554	6 AX045334	AX045334 Sequence
32	514.6	12.9	7554	6 AX463754	AX463754 Sequence
33	514.6	12.9	7554	10 MUSLAM2A	J02930 Mouse lamin
34	464.2	11.6	6055	5 AF468048	AF468048 Danio rer
35	366.8	9.2	551	6 AX302928	AX302928 Sequence
36	350.2	8.8	5184	9 AF041835	AF041835 Homo sapi
37	285.8	7.2	5737	3 DBOLAMB2	M25063 Drosophila
38	284.4	7.1	4482	3 DMLAMB2	X07806 Drosophila
39	265.2	6.6	1778	6 AX335505	AX335505 Sequence
40	265.2	6.6	1778	9 HSLAMI24	U31201 Human lamin
41	265.2	6.6	164084	9 AL354953	AL354953 Human DNA
42	265.2	6.6	170492	2 AL139013	AL139013 Homo sapi
43	263.6	6.6	220000	2 AC004795	AC004795 Homo sapi
44	239	6.0	5153	10 AF083372	AF083372 Mus muscu
45	234.8	5.9	4664	10 AF079520	AF079520 Mus muscu

ALIGNMENTS

RESULT 1	AX045561	5200 bp	DNA	linear	PAT 24-NOV-2000
LOCUS	AX045561				
DEFINITION	Sequence 25 from Patent WO0066731.				
ACCESSION	AX045561				
VERSION	AX045561.1	GI:11344011			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 5200)				
AUTHORS	Boutaud, A.				
TITLE	Recombinant laminin 5				
JOURNAL	Patent: WO 0066731-A 25 09-NOV-2000;				



QY	1712	CTTCGGGGAACTGGCCCAAGTAGAGGCTTGTCAAGCCTGTCACTGACAAACAACAAGCTGGA	1771
Dp	1629	CTTTGGTGAACATGGCCCAAGTAGAGGCTTGTCAAGCCTGTCAATGCAACAGCAATGTGGA	1688
QY	1772	CCCAATAGCCCTCCGGGAAACTGTGACCGCCGTGACAGGAGAGGTGCTGAAGTGCATCCCA	1831
Dp	1689	CCCCAGTGCCTCTGGGAATTTGTGACCGCGCTGACAGGAGAGTGTGTAAGTATCCCAA	1748
QY	1832	CACAGCTTGGGGTCCACATGTGTGACCAAGTCAACAAGCAGGCTACTATGGGGACCCGTTGGCTCC	1891
Dp	1749	CACAGCCGGGACTTACTGTGCGACCAAGTCAACAAGCAGGCTACTTGGGGAGACCCATTGGCTCC	1808
QY	1892	CAATTCAGACAGACAAGTGTGAGGCTTGCACATGCAACCAAGTGGGCTCGAGACCTGTGGA	1951
Dp	1809	CAACCCAGCAACACAAGTGTGAGGCTTCAACTGTAAACCCATGGGCTCAAGAGCTGTAGG	1868
QY	1952	GTCGCAAGTATGGCAGCTGTGTGTTGCAAGCCAGGCTTGTGTTGGTGGCTCAGCTGTGCA	2011
Dp	1869	ATGTGCAAGTATGTGGCACTGTGTGTTGCAAGCCAGGATTTGTGTGCCCACTGTGACGA	1928
QY	2012	TGCGGCACTGACCAAGCTGTCCAGCTTCTATATCAAGTGAAGGTTGATGATCAGTT	2071
Dp	1929	TGGAGCAATT--CAGCTGTCCAGCTTCTATATCAAGTGAAGTATCAGATGATCAGTT	1985
QY	2072	TATCAGACAGTCCAGATCCGTGGAGGGCCGATTTGCAAGGCTCAGG-----TGGAGC	2125
Dp	1986	TATCAGACAGCTTACAGAAATGAGAGCCCTGTGATTTCAAGAGCTCAGAGGTGATGAGGT	2045
QY	2126	AGTACCCACAGCAGAGCTGGAAGGACAGATGACAGCAGGCTGAGCAGGCCCTTCGGACAT	2185
Dp	2046	AGTACCTGATACAGAGCTGGAAGGACAGATGACAGCAGGCTGAGCAGGCCCTTCAGACAT	2105
QY	2186	TCTGAGAGAGCCCGAGATTCCACAAGATGCGTTGATGATCCTTCAATTCGCGGGGCCAA	2245
Dp	2106	TCTGAGAGATGCCCAAGATTTCAGAAAGGTGCTAGCAGATCCCTGTGCTCCAGTTGGCCAA	2165
QY	2246	GGCAAGACCTCAAGAGATATAGCTACCGGAGACCGCTGATGATGACCTCAAGATGACTGTGA	2305
Dp	2166	GGTGAGGAGCCCAAGAAAGACACTACCAAGAGCCGCTGTGATGATCAAGATGACTGTGA	2225
QY	2306	AAGAGTTGGGGCCCTGGGCACTGATACAGAACCAAGTTACAGATCTCGAGGCTCAT	2365
Dp	2226	AAGAGTTGGGGCTGTGGAAATGTACGTACCAAAACGAGTTGCGGATCTCTCAAGGCTCAT	2285
QY	2366	CACACAGATGGGCTGAGACCTGGAGAGAAAGTGAAGCTTCCCTGCAAAAACACCAATTC	2425
Dp	2286	CACTCAGATGAGCTGAGCCTGGCAGAAAGTGAAGCTTCTTGGGAAACACTAACATTC	2345
QY	2426	TCCTTCAGAGCACTACGTGGGGCCAAATGCGTTTAAAAAGTCTGGCTCAGAGAGCCACGAG	2485
Dp	2346	TGCTTCAGAGCACTACGTGGGGCCAAATGCGTTTAAAAAGTCTGGCTCAGAGAGCCACAG	2405
QY	2486	ATTGGAGACAGCCATGTTCACTGATGAGCAGTAAACATGAGAGCAACTGGCAAAAGGAAACCA	2545
Dp	2406	ATTGACGAAAGACCACTGTGATGATGAGCAGTAAACATGAGAGCAACTGGCAAGGAAACCTGA	2465
QY	2546	GGAGTATTTCCAAAGAGTGTACTGTGTCGGAGGCTCTCTGCAGAGAGAG-----G	2599
Dp	2466	GGACTATTTCCAAAGAGCCCTCTCACTGATGTGCGAAGGCCCTGCTATGAGAGTCCGGAAG	2525
QY	2600	CGGAAGGCGGACCTGGACCGGAGCCGTGTGTCAAAAGGCTTGTGGGAAAAATTTGCGAAAAAC	2659
Dp	2526	CGGAAGGCGGTGACCCCGAGCGGTGTGTGTGTCAAAAGGCTTGTGGAAAAATTTGGAGAAAC	2585
QY	2660	TAAATCTCTGCCCCAGAGTGTGTGAGGAGAGGCCACGCAACACACATGGAAGCAGATAG	2719
Dp	2586	CAAGTCCCTGGCCAGACAGTGTGACAAGGAGGCCACTCAACGGGAATTTGAAGCAGATAG	2645
QY	2720	GTCATTATCAGATAGTCTCACACTTCTCAATTCCTGCTGTCTCAGATTCAGGAGTCAATGA	2779
Dp	2646	GTCATTATCAGACAGTCTCCGCTCTCTGAGATTCAAGTGTCTCCGCTCAGGAGGACAGGA	2705

QY	2780	TCAGTCCCTTGCAGGT - - AGAAGCAGAGAGGCTCAGACAAAAAGCTGATTCCTCTCAAA	2836
Db	2706	TCAGTCCCTTGCAGGTGGAAGGAAGCAAAAGAGTCAAAAGGAGGATTTCACTCTCAAG	2765
QY	2837	CCGTGTGACTAAGCATATGATGATAGTTCAACAGCTGCAGAAACATCGGAGAACTGGGA	2896
Db	2766	CCTGTTAACACAGGCATATGATGATGATTCACACAAAGAAATCTGGGAAACTGGAA	2825
QY	2897	AGAAAGAAACCCGGCAGCTCTTACAGAAATGGAAGAATGGGAGACAGATCAGATCAGCT	2956
Db	2836	AGAAAGAAACACAGCAGCTCTTACAGAAATGGAAGAAAGTGGGAGAGAAATCAGATCAGCT	2885
QY	2957	GCTTCCCGCTGCCAACCTTGCCTAAAGAGAGCCCAAGAACCACTAGTATGGGCATATGC	3016
Db	2886	GCTTCCCGCTGCCAACTTTCCTAAAGAGAGCCCAAGAACCACTAGTATGGGCATATGC	2945
QY	3017	CACCTTTATGAAAGTTGGAACATCTTAAACAAATCTCAGAGAGTTTGACCTGCAGAGTTGG	3076
Db	2946	CACCTTTATGAAAGTTGGAAGCATCTTAAACAACTCAGAGAGTTTGACCTGCAGAGTTGG	3005
QY	3077	AGATTAAGAGCAGAGCTGAAAGAGCCATGAGAGACTCTTCATCATCAGCCAGAAAGT	3136
Db	3006	CAACGAAAGACAGAGCTGGAAGAGCCATAGAGACTCTTCATCATCAGCCAGAAAGCT	3065
QY	3137	TGCAGTGCACAGTGCAGAGCAAGCAGAAACAGCCCTGGGCACTGCTGTCGCCGA	3196
Db	3066	TTTCAGATGCCAGTGCAGAGCAAGCAGAAAGAGCCCTGGGAGAGCGCTGCTGCTGA	3125
QY	3197	CGCCAGAGGGCAAGAAATGCAGCCAGGAGGCGCTGAGATCTCTGGCAAGATAGACA	3256
Db	3126	TGCACAGAGGGCAAGAAATGAGGGCGCGGAGAGCGCTTGAAATCTCAGATGAGATTAACA	3185
QY	3257	GGAGATTAGAGGTCGTAACCTTGGAAAGCCAAATGTGCACAGTGGAGGCTTGGGCATAGA	3316
Db	3186	GGAGATTGGAGTCTGAACTTGGAGGCCAAATGTGCACAGTGGAGGCTTGGGCATAGA	3245
QY	3317	GAAGGAGCTGGCCACTCTGAAAAGTGAGATGAGAGAACTGGAAGAGAGCTGTCAAGAA	3376
Db	3246	AAAGGAGCTGGCCCTCTCTGAAAGTGAGATGAGGGAAGTGGAAAGAGAGCTGTCAAGAA	3305
QY	3377	GGAGCAGAGATTGACATGATGTAGAGCAGCTGCAGATGTGAATGTGAGAGGCCCAAG	3438
Db	3306	GGAGTGGAGTTTGACAGAAATGTGAATGAGTACAGATGTGGATTACAGAGGCCAACA	3365
QY	3437	AGTTGAAAACAGAGCCAGAATGTCTGAGAGTTACGATCCAGACACTCAACACATTGGA	3498
Db	3366	GTTTATACAGAGCCAGAAAGCTGGGGTTTACATCCAAAGCAGACTCAACACATTGGA	3428
QY	3497	TGGCATCCTACACTAATAGACAGCCCTGGCAGTGTGATGGAAGAGAGGCTGATCTTACT	3558
Db	3426	CGGCTCCTCGATCTGATGTAGACCAAGCCCTCAGTGAATGTAAGTAAGAGGGGCTGTCTTACT	3485
QY	3557	GGAGAGAGAAAGCTTTCCGAGGCCAAGTCAAGTCAACAGCCAGCAGAGGCCCTTATATGC	3618
Db	3486	GGAGAGAGAAAGCTTTCCGAGGCCAAGTCAACAGCCAGCAGACTCGGGCCATATATGC	3545
QY	3617	AGAGCTGGAAGAGAGGCAATCGGACAGAAAGGCCACTCGCTTCTGTGAGACTAGCAT	3677
Db	3546	AGAGCTGGAAGAGAGGCAATCGGACAGAAAGGCCACTCGCTTGTGAGAGACTAGCAT	3606
QY	3677	AGATGGGATTTGCGCTGATGTGAAGAACTGGAAGAACTCAGGAGCAACTGGCCCCGGG	3738
Db	3606	AGATGGGATTTGCGCTGATGTGAAGAACTTGGAGAACTTGAAGGCAACCTGGCCCCAGG	3665
QY	3737	CTGCTACAAATACCCAGAGCTCTTGAGCAACAGTGAAGCTGCCCTTAAGATTTCTCAACCA	3798
Db	3666	CTGCTACAAATACCCAGAGCTCTTGAGCAACAGTGAAGCTGCCCTTAATTTCTCAACGA	3728
QY	3797	GGTCTTGGGATTCAGACCTAGCTGCCTTAGAGATTTCTCA	3837
Db	3726	GGTCTTGGGATTCAGATCTCAGGCGCTGGGAGGCATCTCA	3766

[illegible]

Db	732	TAAGATCACTCTACCTTTCATCAAGATGTTGATGCGTGGAAAGCTGTCCAAACCAATATG	791
OY	872	GTCCTCTGCAAGGCTCCAGTGGTCACACAGCGCATCGGATATATTTAGCTCAGCAGCAG	931
Db	792	GTCCTCTGCAAGGCTCCAAATGTCACACAGCGCATCAAGATGTGTTTAGCTCAGCCAAAG	851
OY	932	ATCAGACCCCTGTATTTTGTAGCTCCCTGCCAAATTTCTTGGAAATCAACAGGTGAGCTA	991
Db	852	ACTGATCTCTGTATTTTGTGGCTCCGCCAAATTTCTTGGGAATCAACAGGTGAGCTA	911
OY	992	CGGGCAAAAGCCTATCTTTTGTGACATCCGCTGATGAGGGGAGGAGCAGACCCATCTGCCA	1051
Db	912	TGGGCAAAAGCCTGTCTTTTGTGACTACCGTGTGACAGAGAGGAGCAGACCCATCTGCCA	971
OY	1052	TGAGCTGATCTCGAAGGTTGCTGCTACAGGATCAGACGCTCCCTTGATGTCACATTCAGAA	1111
Db	972	TGATGTGATCTCGAAGGTTGCTGCTACAGGATCAGACGCTCCCTTGATGCCACTTGGCAA	1031
OY	1112	GACACTGCTTTGTGGGATCCACCAAGACTTACACATTCAGATTAAATGACATCCAAAGC	1171
Db	1032	GACACTGCTTTGTGGGCTCACCAAGACTTACACATTCAGTTAAATGACATCCAAAGCA	1091
OY	1172	TAATTTGGAGCCCCAGCTAAGTTACTTGTGATATCGGGGTTTACGCGGAATCTCACAGC	1231
Db	1092	TAATTTGGAGCCCCAGCTGAGTTACTTGTGATATCGAAGGTTTACTGCGGAATCTCACAGC	1151
OY	1232	CCTCGGATCCGAGCTACCTACGAGAGATACAGTACTGGGTACATTCAGAACGTGACTT	1291
Db	1152	CCTCGGATCCGAGCTACATATGAGAAATACAGTACTGGGTACATTCAGAAATGTGACCT	1211
OY	1292	GATTTTCAAGCCCGCCCTTTCTTGAGACCCACAGCCGCTGGGTGACAAATGTATGCC	1351
Db	1212	GATTTTCAAGCCCGCCCTGTCTCTGAGAGCCCAACCCCTGGGTTGACAGTGTAAATGTTC	1271
OY	1352	TGTTGGCTACAAAGGGGCGATCTCCGAGAGATGTGCTCCGGGCTACAAAGAAAGATTCAGC	1411
Db	1272	TGTTGGGTACAAAGGGGCAATTCCTCCAGAGATGTGCTTCTGCTACAAAGAAAGATTCAGC	1331
OY	1412	CAGACTGGGACCTTTTGGCACCTGTATTCATGTAACTGCCAAAGGGGAGGGGCTCGCA	1471
Db	1332	GAGACTGGGGGCTTTTGGCACCTGTATTCCTTTGAACTGTCAAGGGGAGGGGCTCGCA	1391
OY	1472	TCCAGACACAGAGACTGTTACTCAGAGGGATAGAACCTTGACATCCCTGAGTGTCTGA	1531
Db	1392	TCCAGACACAGAGAAATGTGTTATTCAGGGGATGAAATCTCTACAT--TGAGTGTGCTGA	1448
OY	1532	CTGGCCCATGTTGTTTCTACACAGATTCACAAGACCCCGGAGCTGCAAGCGGTGCCCTG	1591
Db	1449	CTGGCCCATGTTGTTTCTACAAAGATTCGCAAGACCCCGGAGCTGCAAGCGCATGTCCCTG	1508
OY	1592	TCCGAATAGGTTACAGCTGCTCCGATGATCCCTGAGACAGAGAGGTTGTTGCAATTAATG	1651
Db	1509	TCAATACGGGTTACAGCTGCTCAGTGATTTCCGGAAGACGAGAGGTTGTTGCAATTAATG	1566
OY	1652	CCCCCAGGGTTCACGTGGTGCCGCTGTGACTGTGTGATGAGCTATTTTGGGAGCC	1711
Db	1569	CCCCCAGGGGTTACCGGTGCCCCGCTGTGACTGTGTGATGAGCTATTTTGGGAGCC	1628
OY	1712	CTTGGGGGAACGTGGCCCAAGTAGAGGCTTGTACACCCCTGTACGTGCAACCAACAGTGGGA	1771
Db	1629	CTTGGGTGAACATGGCCCAAGTAGAGGCTTGTACACCCCTGTAAATGCAACACCAATATGTGA	1688
OY	1772	CCCTAATGTCCTCCGGGAATCTGACACGGCTTACAGGAGGAGGTCTGAAGTCTATCAACAA	1831
Db	1689	CCCCATGTGCTCTGTGGGAATTTGTACACGGCTTACAGGAGGAGGTCTTGAAGTATTCACAA	1748
OY	1832	CACAGCTGGGGTCCACTGTGACACAGTGCAAAGCAGGCTACTAATGGGAGCCGTTGGCTCC	1891
Db	1749	CACAGCGGGATCTACTGTGCGACGAGTGCAAGGCTACTTGTGGGAGCCCATTTGGCTCC	1808
OY	1892	CAATTCAGACAGACAGTGTGAGCTTGCACATGCACCCAGTGGGCTTCGAGACCTGTGGGA	1951



Db 1809 CAACCCACAGACAAAGTGTGAGCTTGCACACTGTAAACCCATGAGCCTCAGACCTGTAGG 1868  
QY 1952 GTGTGAGATGATGAGCAGCTGTGTGCAAGCCAGCCTTTGTGGCCCTCAGCTGTGACCA 2011  
Db 1869 ATGTGAAGTATGATGACCTGTGTGCAAGCCAGATTTGTGGCCCACTGTGACCA 1928  
QY 2012 TCGCGCACTGACAGCTGCTCCAGCTTGTCTATATCAATGAGTGAAGTTCAGATGATGAT 2071  
Db 1929 TGGAGCATTT---CAGCTGTCCAGCTTGTCTATATCAATGAGTGAAGTTCAGATGATGAT 1985  
QY 2072 TATGACAGACCTCCAGATCTGTGAGAGCCCTGTATTTGCAAGGCTCAGGG-----TGAAGC 2125  
Db 1986 TATGACAGACCTCCAGATGAGAGAGCCCTGTATTTCAAGGCTCAGGGGTGAGTGAAGT 2045  
QY 2126 AGTACCAGACGAGAGCTGGAAGGAGATGACAGAGCTGACAGAGCCCTTCCGGACAT 2185  
Db 2046 AGTACCTATACAGAGCTGGAAGGAGATGACAGAGCTGACAGAGCCCTTCCAGACAT 2105  
QY 2186 TCTGAGAGAGCCAGATTTTCAAGATGCTGTATGATCTTCAATCTCCGGGTGGCCAA 2245  
Db 2106 TCTGAGATGCGCCAGATTTCAAGAGTGTAGACAGATCCCTGTGCTCCAGTTGGCCAA 2165  
QY 2246 GCGAAGACCTAAGAGATAGCTACCGGAGCCGCTGTGATGACTCAAGATGACTGTGA 2305  
Db 2166 GGTGAGGAGCCAGAGAACACTACAGAGCCGCTGTGATGACTCAAGATGACTGTGA 2225  
QY 2306 AAGAGTTGCGGCGCCGAGCAGTATACAGAACCAATGACAGTACTCCGAGGCTCAT 2365  
Db 2226 AAGAGTTGCGGCTGTGGAGAGTCACTACAGAACCGAGAGTGGAGTACTCACAGGCTCAT 2285  
QY 2366 CACTCAGATGCGCCTGTGAGAGAAAGTAGAGCTTCCCTGCAAAAACACCAACATTTCC 2425  
Db 2286 CACTCAGATGAGAGCTGTGAGAGTGTGAGAGAAAGTGAACCTTCCCTGGAAACACATCAATTTCC 2345  
QY 2426 TCTCTCAAGACACTACGTGGGGCCCAATGCTTTAAAGTCTGCTCAGAGGCCACGAG 2485  
Db 2346 TGCCTCAAGACACTACGTGGGGCCCAATGCTTTAAAGTCTGCTCAGAGGCCACGAG 2405  
QY 2486 ATTGCGACAGACGCTGTGAGTGTGAGCAGTAACTGAGCAGACAGCCAGAAAGCAACCA 2545  
Db 2406 ATTGCGACAGAAACCGCTGTGAGTGTGAGCAGTAACTGAGCAGACAGGAAACTGTA 2465  
QY 2546 GGAGTATTTCCAAAGAGCTGATGTCACTGTGGCGAGGCTGTGACAGAGAG-----G 2599  
Db 2466 GGAGTATTTCCAAAGAGGCGCTGTCACTGTGGCGAGGCGCTGTGAAAGAGTGGAGAG 2525  
QY 2600 CGGAAGCGGACGCTGTGAGAGGAGCCGTGTGCAAAAGCTTGTGGCAAAATTTGCAGAAAC 2659  
Db 2526 CGGAAGCGGAGCCCGAGAGGCTGTGTGTCAGAGGCTTGTGCAAAATTTGAGAAAAAC 2585  
QY 2660 TAAATCTGTGGCCCGAGAGTGTGTGAGGAGGCGCAGCAACCGACATGGAAGCAGTATG 2719  
Db 2586 CAAAGTCCCTGGCCCGAGAGTGTGACAAAGGAGGCGCACTCAAGCGGAAATTTGAAGCAGATG 2645  
QY 2720 GTCTTATCAGATAGTATCTCAACCTTCAATTCCTGTCTCAGATTCAGAGGAGTAAATGA 2779  
Db 2646 GTCTTATCAGACACTCTCCGCTCTCGATTCATGTGTCTCCGCTTCAGAGGAGTCAGTGA 2705  
QY 2780 TCAGTCTTGCAGGT---AGAAAGCAAGAGGCTCAGACAAAAAGCTGATTTCTCTCAAA 2836  
Db 2706 TCAGTCTTTCAGGTGGAAGAGCAAGAGAGATCAAAAGAGGAGATTCCTACTCTCAAG 2765  
QY 2837 CCGTGTGACTAAGCATTATGAGATGATTCAGACAGCTGCAAAAGCATCTGTGGAAACTGGGA 2896  
Db 2766 CTTGTATACCAAGCATTATGAGATGATTCAGAGCTTCAAGCGTACCAAAAGAAATCTGGGAACTGGAA 2825  
QY 2897 AGAAGAAACCCGAGCTCTTACAGATGGAAGAATGGAAGAGACAGACATCGATCAGACT 2956  
Db 2826 AGAAGAAAGACAGAGCTCTTACAGATGGAAGAAAGTGGAGAGAGAAATCAGATCAGCT 2885  
QY 2957 GCTTTCCGTCGCAACTTGTCTAAAGCAGAGCCCAAGAGACCTAAGTATGAGGCAATGC 3016  
Db 2886 GCTTTCCGTCGCAACTTGTCTAAAGCAGAGCACAAGAACATGAGTATGAGGCAATGC 2945

QY 3017 CACTTTTATGAGTGTGAAGACATCTTAAAGATCTAGAGAGTTGACTGCAAGTTGG 3076  
Db 2946 CACTTTTATGAGTGTGAAGACATCTTAAAGACCTCAGAGAGTTGACTGCAAGTTGA 3005  
QY 3077 AGATAAAGAGCAGAGCTGGAAGAGGCGCATGAGAGACATCTCTCATCAGCAGAAAGT 3136  
Db 3006 CAACGAAAGAGAGAGCTGAAGAAAGCATGAGAGAGATCTCTCATCAGCAGAAAGT 3065  
QY 3137 TGCAGTCCAGTGTACAGAGCAGAGCAGAGACAGCCCTGGCAGTGTCTGCTGCCGA 3196  
Db 3066 TTCAGATCCAGTGTACAGAGCAGCAGAGAAAGAGCCCTGGGAGCGCTGTCTGTGA 3125  
QY 3197 CGCCGAGAGGCGAAAGATGACAGCCAGGAGGCGCTGTGAGATCTCTGCGAAGATTAACA 3256  
Db 3126 TGCACAGAGCGAAAGATGGGGCCGGGAGGCGCTGTGAAATCTCTCAGTGTGATTAACA 3185  
QY 3257 GGAGATAGAGAGTCTGAACCTTGAAGCCCAATGTGACAGCAGATGAGAGCTTGGCCATGGA 3316  
Db 3186 GGAGATAGAGAGTCTGAACCTTGAAGCCCAATGTGACAGCAGATGAGAGCTTGGCCATGGA 3245  
QY 3317 GAAGGAGTGGCTCTGTGAAGAGTGAAGATGAGAAATGGAAGAGAGCTGTCAAGGA 3376  
Db 3246 AAAGGAGTGGCTCTGTGAAGAGTGAAGATGAGGAAAGTGAAGAGAGCTGTGAAGGA 3305  
QY 3377 GGAGCAGAGGTTTGCATGATGATGAGAGCAGATGAGATGGTAATTTGAGAGAGGCCAAG 3436  
Db 3306 GGAGCTGTGAGTTTGCACAGATATGATATGACATACAGATGGTATTTACAGAAAGCCACGA 3365  
QY 3437 AGTTGAAAAACAGAGCCAGAAATGCTGAGATTACGATTCAGACACACTCAACATTTGA 3496  
Db 3366 GGTGATATCCAGAGCCAGAAAGAGCTGTGGGTTTACATTTCCAAAGCACATCAACATTTGA 3425  
QY 3497 TGGCATCTCTACCTTAATAGACACAGCTGTGCAAGTGTGATGAAGAGAGCTGTACT 3556  
Db 3426 CGGCTCTCTGATCTGATGAGACACAGCTCTCAGTGTATGATGAAGAGGCGCTGTACT 3485  
QY 3557 GGAGCAGAGGTTTCCGAGCCAGACAGTCAAGACAGCCAGCTACGCGCCCTGATGTC 3616  
Db 3486 GGAGCAGAGGTTTCCGAGCCAGACAGTCAAGACAGCCAGCTACGCGCCCTGATGTC 3545  
QY 3617 AGAGCTGGAAGAGAGGACATCGGACAGAGGCGCACCTCGCTTCTGTGAGACTAGAT 3676  
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QY 3677 AGATGGATTTCTGCTGATGTGAAGACCTGTGAGAACTCAGGAGCAACTGCCCCGGG 3736  
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QY 3737 CTGTACAAATACCGAGGCTCTGTGACACAGTGAAGCTGCTTAGAGATTTCTCAACAA 3796  
Db 3666 CTGTACAAATACCGAGGCTCTGTGACACAGTGAAGCTGCTTAGAGATTTCTCACTGA 3725  
QY 3797 GGTCTTGGGATTCAGACCTAGCTGCTTAGAGATTTCTCA 3837  
Db 3726 GGTCTTGGGATTCAGACATCTCAGGCTGTGGAGGCGCATGTGA 3766

RESULT 3  
HSLAMB2T  
LOCUS H.sapiens mRNA for laminin. 5200 bp mRNA linear Pri 27-MAR-1996  
DEFINITION  
ACCESSION Z15008.S47028  
VERSION Z15008.1 GI:34229  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE  
1 (bases 1 to 5200)  
Kallunki,P., Sainio,K., Eddy,R., Byers,M., Kallunki,T., Sariola,H.,  
Beck,K., Hironen,H., Shows,T.B. and Tiryagverson,K.  
A truncated laminin chain homologous to the B2 chain: structure,  
TITLE





QY 3677 AGATGGATTCGCTGATGTGAAGAAGAACTGGAGAAATCAGGGAACCTGCCCGGG 3736  
DB 3606 AGATGGATTCGCTGATGTGAAGAAGAACTGGAGAAATCAGGGAACCTGCCCGGG 3665  
QY 3737 CTGCTCAATTAACAGGCTCTTGAGCAACAGTAAGCTCTAGAGATTTCACACCA 3796  
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DB 3726 GATTCTTGGGATTCAGACCTAGCTGCTTGAAGATTTCCTCA 3766

RESULT 4  
AX365737 5156 bp DNA linear PAT 15-FEB-2002  
LOCUS Sequence 130 from Patent WO0200174.  
DEFINITION AX365737  
ACCESSION AX365737  
VERSION AX365737.1 GI:18697286  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE  
AUTHORS Wang, T., Wang, A., Skelky, Y. A., Li, S. X., Kalos, M. D., Henderson, R. A.,  
1 Mammalian, P. D., Fanger, N., Retter, M. W., Marnerakis, M., Fanger, G. R.,  
Vedell, T. S., Carter, D., Watanabe, Y., and Pechham, D. W.  
TITLE Compositions and methods for the therapy and diagnosis of lung  
cancer  
JOURNAL Patent: WO 0200174-A 130 03-JAN-2002;  
FEATURES  
source CORIXA CORPORATION (US)  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"

BASE COUNT 1351 a 1222 c 1377 g 1206 t  
ORIGIN

Query Match 74.1%; Score 2956.4; DB 6; Length 5156;  
Best Local Similarity 88.4%; Pred. No. 0;  
Matches 3285; Conservative 0; Mismatches 401; Indels 28; Gaps 6;

QY 146 CGAGGCGCGGCGAGCGAGCCCTGACGCGCG-----GACGCGCGCGCGCGCTTGCA 198  
DB 7 CGAGGCGCGGCGAGCGAGCCCTGACGCGCGAGACAGACTGAGCGCGCGCGCGCGCA 66  
QY 199 TGGCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 258  
DB 67 TGGCTCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126  
QY 259 CCACCTCGGAGGAGGAGTCTGTGATTGCAAGCGGAGATCCAGCAATGATCTTGGAC 318  
DB 127 CCACCTCGGAGGAGGAGTCTGTGATTGCAATGAGGAGTCCAGGAGTGTATTTGATC 186  
QY 319 AGGAATTCACAAACAGAGAGAAATGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 378  
DB 187 GGAATTCACAAACAGAGAGAAATGATTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 246  
QY 379 ATGGCATTCACATGCGAGAGTGTGAGGAGGAGATTTTACGACAGAGAGAGAGAGCGCT 438  
DB 247 ATGGCATTCACATGCGAGAGTGTGAGGAGGAGATTTTACGAGAGAGAGAGAGCGCT 306  
QY 439 GTTACCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 498  
DB 307 GTTACCTGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 366  
QY 499 GGTGCGCTGTAAAGCAGGTGTGACAGAGAGAGAGAGAGAGATGCTGCGCGGCTTC 558  
DB 367 GGTGCGCTGTAAAGCAGGTGTGACAGAGAGAGAGAGAGAGATGCTGCGCGGCTTC 426  
QY 559 ACACACTCACTGATGTGGGTGGCGCCCAAGACCAAGGCTGCTAGACTCCAAAGTGTACT 618

DB 427 ACAATGCTCAAGATGCGGGGTGACACCAAGACAGAGACTGCTAGACTCCAAAGTGTACT 486  
QY 619 GTGACCCAGCTGATCTGATGAGGAGGCTGTGAGTCAAGGCGCTGTGCTGCAAGCGGCTG 678  
DB 487 GTGACCCAGCTGATCTGATGAGGAGGCTGTGAGTCAAGGCGCTGTGCTGCAAGCGGCTG 546  
QY 679 TCACCTGAGAGCGCTGTGATGAGTGTGACAGAGATTACTATCACTGATGAGGAGAGAC 738  
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DB 907 ACCATCTGCCATGATGATGATCTGGAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 966  
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QY 1219 GGAACCTCAAGAGGCTGCGGATTCGAGTCACTACGAGAAATACACTGCTGCTGATTTG 1278  
DB 1087 GGAATCTCAAGAGGCTGCGGATTCGAGTCACTACGAGAAATACACTGCTGCTGATTTG 1146  
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QY 1399 AAAGAGATTCAAGCAGTGGGACCTTTTGGACCTGTATTCATGATTAATGCAAGGAG 1458  
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DB 1327 GAGGAGCTGCTGATTCACAGAGAGAGTGTATTCAGGAGTGAAGCCCTGATATCC 1384  
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DB 1385 -TGAGTGTGCTGATCCCATTTGTTTGTATTAACAGATCCCAAGAGCCCGCAGCTGCA 1443  
QY 1579 AACCGTGCCTGTGCAATGAGGATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1638  
DB 1444 AGCATGATCCCGTGTATTAACAGGATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 1503  
QY 1639 TGTGCAATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1698

Db	1504	GTGCAATAACTGCCCTCCCGGGGTACACGGTGGCCCGCTGTGAGCTCTGTGCTATAGGCT	1503
OY	1504	ATTTTGGGGACCCCTTGGGGGAAGTGGCCCACTGAGAGCCCTTGTCAAGCCCTGTCACTGCA	1758
Db	1564	ACTTTGGGGACCCCTTGTGTGTAACATGGCCCACTGAGAGCCCTTGTCAAGCCCTGTCAATGCA	1623
OY	1759	ACAACAACTGTGGACCCCTTATGTGCTCCCGGGAACTGTGAACCGCTGTCAAGGCAAGGTGTCTGA	1818
Db	1624	ACAACAACTGTGGACCCCAAGTGCCTCTGTGGGAATTTGTACCGGCTGTACAGGCAAGGTGTGGA	1683
OY	1819	AGTGCATCCAAACAACAAGCTGGGGGTCCACTGTGACCAAGTGAACGAGAGGCTACTATAGGGG	1878
Db	1684	AGTGTATCCAAACAACAAGCGGGCATCTACCTGACCAAGTGAACGAGGCTACTATCTGGGG	1743
OY	1879	ACCGGTTGGGCTCCCAATTCACAGCAACAAGTGTCAAGCTTGGCACTGTGCAACCCATGGGCT	1938
Db	1744	ACCATTTGGGCTCCCAACCCACAGCAACAAGTGTCAAGCTTGGCACTGTGCAACCCATGGGCT	1803
OY	1939	CGAAGCCTGTGGAGTGTGGAATGTATGGGCACTGTGTGTTGCAACCAAGGCTTTGGTGCC	1998
Db	1804	CAGAGCCTGTGTAGTGTGTGGAATGTATGGGCACTGTGTGTTGCAACCAAGGATTTGGTGCC	1863
OY	1999	TCAGCTGTGACATAGCGGCACTGTGACCAAGCTGTCCAGCTTGCCTATATATCAATGAAAGTTC	2058
Db	1864	CCAAGCTGTGACATAGGACATTT---CAAGTGTCCAGCTTGCCTATATATCAATGAAAGTTC	1920
OY	2059	AGATGATCACTATTATGACAGAGCTCCAGATCTGTGAGGCCCTGATTTTCGAAGCCTCAGG	2118
Db	1921	AGATGATCACTATTATGACAGAGCTCCAGATCTGTGAGGCCCTGATTTTCGAAGCCTCAGG	1980
OY	2119	G-----TGAGACATACCCCAAGCAGAGCTGGAAGGCAAGGATCAGCAGGCTGAGCAGG	2172
Db	1981	GTGCTGATGAGTGTAGTACTGATACAGAGCTGGAAGGCAAGGATCAGCAGGCTGAGCAGG	2040
OY	2173	CCCTTCGGGCAATCTGTGAGAGAACCCAGATTTTCAACAAGATGCTGTATGATCTCTCAATC	2232
Db	2041	CCCTTCAGAGCAATCTGTGAGAGATCCCAAGATTTTGAAGAAGTGTACGACAGATCCCTTGCTC	2100
OY	2233	TCCGGGTGGCCCAAGGCAAGCACTCAAGAGATACCTACCGGGACCGCTGTGATACCTCA	2292
Db	2101	TCCAGTTGGCCCAAGGTGAGAGCCCAAGAAGAACACTACAGAGCCGCTGTGATACCTCA	2160
OY	2293	AGATGACTGTGGAAGAAGTTCGGGCCCTGGGCACTCAAGTATCAGAACCCAACTTCAGGATA	2352
Db	2161	AGATGACTGTGGAAGAAGTTCGGGCCCTGGGCAAGTATCAGAACCCAACTTCGGGATA	2220
OY	2353	CTCCGAGGCTATACACTCAAGTGTGGGCTGTGAGCCTGTGAGAGAAAGTAGGCTTCCCTGCATA	2412
Db	2221	CTCAGAGGCTATACACTCAAGTGTGAGCCTGTGAGAGAAAGTAGGCTTCCCTTGGGATA	2280
OY	2413	ACACCACATCTCTCTTCAGAGCACTGTGTGGGGCCAAATGGGCTTTTAAAAGTGTGGGCTC	2472
Db	2281	ACACTAATCTCTCTCTTCAGAGCACTGTGTGGGGCCAAATGGGCTTTTAAAAGTGTGGGCTC	2340
OY	2473	AGGAGGCCACAGATTGGCAGACAGCCATGTTCACTGATGAGCCAGCTAATGTGAGCAACTGG	2532
Db	2341	AGGAGGCCACAAAGATTAGCAGAAAGCCAGTTGAGTGCAGCCAGTAACTGTGAGCAACTGA	2400
OY	2533	CAAGAGAAACCCAGAGAGTATTCCAAAGAGCTGATGTCACTGTGTGCGAGGCTGTGCAGG	2592
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OY	2593	AAGGAG-----GGGAGAGCGGCAAGCCTGTGAGCGGAGCGGCTGTGTGGAAGGGCTTGGGGAA	2648
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OY	2647	AATTCAGAAATCTCTCTGTGGCCACAGAGTTGTGAGAGGAGAGCCACGCAAAACCGACA	2706
Db	2521	AATTCAGAAATCTCTCTGTGGCCACAGAGTTGTGAGAGGAGAGCCACGCAAAACCGACA	2580
OY	2707	TGGAAGCAGATAGGCTTATCAGCATAGTCTTCACACTTCTCAATTCCTGTCTCAGATTC	2766
Db	2361	TTTGAAGCAGATAGGCTTATCAGCATAGTCTTCACACTTCTCAATTCCTGTCTCAGATTC	2640

QY	2767	AGGAGATCAATGATCAGTCCTTGGACGT--AGAAAGCAAAAGGCTCAGACAAAACCTG	2823
Db	2641	AGGGAGTCAAGATCAGTCCTTGAAGTGGAAAGAAAGCAAAAGAGATCAAAACAAAACGG	2700
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Db	2701	ATTCACTCTCAAGCTGGTAAACAGGCAATTATGATGAGTTCAACGCTACAGAAAGATC	2760
QY	2884	TGGAAACTGGGAAGAAAGAACCCGGCAGCTCTTACAGATGGAAGAATGGAGACAGA	2943
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QY	2944	CATCAGATCAGCTGCTTCCCGTCCCAACCTGCTAAAGCAGAGCCCAAGAACACTAA	3003
Db	2821	AATCAGATCAGCTGCTTCCCGTCCCAACTGCTTAAAGCAGAGCAACAAAGAACCTCGA	2880
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Db	2881	GTATGGGCAATGCCACTTTTATATAGTTTGAAGACATCTTAAAGAAATCTCAGAGATTG	2940
QY	3064	ACCTGACAGTTTGGAGATTAAGAGACAGACTGAAGAGGCCATGAAGAGACTCTCTTCA	3123
Db	2941	ACCTGACAGTTTGGAGATTAAGAGACAGACTGAAGAGGCCATGAAGAGACTCTCTTCA	3000
QY	3124	TCAGCCAAAGTTTGCAGGTGCCAGTGCACAGACGAAGCAAGCAAGACAGACCTGGGCA	3183
Db	3001	TCAGCCAAAGTTTGCAGGTGCCAGTGCACAGACGAAGCAAGCAAGACAGACCTGGGGA	3060
QY	3184	GTGCTGTCGCGACGCCAGAGGGCAAGAAATGCAGCCAGGAGGCCCTGGAGATCTCTG	3243
Db	3061	GGCGTGTCTGATATGCACAGAGGGCAAGAAATGGGGCCGGGAGGAGCCCTGGCAATCTCA	3120
QY	3244	GCAAGATTTGAACAGAGATTAGAGGCTCGAATCTTGAAGCCCAATGTGCACACAGATGGAG	3303
Db	3121	GTGAGATTGAACAGAGATTTGGAGCTCTGAACCTTGGAGCCCAATGTGCACACAGATGGAG	3180
QY	3304	CCTTGGCCATGGAGAGGGAGCTGGCAGCTCTGAAAAAGTGAAGATGAGAAATGGAAAGAG	3363
Db	3181	CCTTGGCCATGGAGAGGGAGCTGGCCTCTGAAAGATGAGAAATGGAAATGGAAAGAG	3240
QY	3364	AGCTGTCAAGGAAGAGACGAGAGATTGACATGATGATGAGACGAGTGCAGATGGTAATT	3423
Db	3241	AGCTGTCAAGGAAGAGAGCTGGAGTTTGACAGCAATGATGATGAGACGATGCAGATGGTATTA	3300
QY	3424	CAGAGGCCCAAGAGATTGAAAAACAGAGCCCAAGAAATGCTGGAGTTACGATCCCAAGACAC	3483
Db	3301	CAGAGGCCCAAGAGATTGATACAGAGCCCAAGAAACGCTGGGGTTTACATCCAAAGCACAC	3360
QY	3484	TCACACATTTGGATGTCATCTTACACTTAATAGACAGCTTGGCAGTGTGATGAAGAGA	3543
Db	3361	TCACACATTTGGATGTCATCTTCTGCTGATGAGACAGCCCTCCTAGTATGATGAAGAGG	3420
QY	3544	GGCTATCTTACTGGAGAGAAAGCTTTTCCAGGCCAAACATCAGATCAACAGCAGCTAC	3603
Db	3421	GGCTATCTTACTGGAGAGAAAGCTTTTCCAGGCCAAGACCCAGATCAACAGCCAACTGC	3480
QY	3604	GGCCCTTGATGTCAAGAGCTGGAAGAGAGGGACATGGCAGAAAGGGCCACTCCCTTCC	3663
Db	3481	GGCCCTTGATGTCAAGAGCTGGAAGAGAGGGACATGGCAGAAAGGGCCACTCCATTTGC	3540
QY	3664	TGGACATTCGATTAATGAGGANTCTGGGTGATGATGTAACACCTGGAGAACATCAGGGGCA	3723
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QY	3724	ACCTGCCCCGGGGCTCTACAAATACCAGGGCTCTTGGACCAACAGTGAAGCTCCCTTAAG	3783
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QY	3784	ATTTTCAACCAAGGTTCTTGGGATTCAGACCTTACGCTCTTAAAGATTTCTCA	3837
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LOCUS	HSNICE	5156 bp	mRNA	linear	PRI 02-FEB-1994
DEFINITION	H.sapiens mRNA for nicein B2 chain.				
ACCESSION	X73902				
VERSION	X73902.1	GI:452754			
KEYWORDS	basement membrane; laminin; nicein; structural protein.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 5156) Valliy,J., Verrand,P., Champliand,M.F., Gereche,D., Magman,D.W., Bauloin,C., Aberdam,D., Burgeson,R., Bauer,E. and Ortonne,J.P.				
TITLE	The 100-kDa chain of nicein/kallin is a laminin B2 chain variant				
JOURNAL	Eur. J. Biochem. 219 (1-2), 209-218 (1994)				
MEDLINE	94139694				
PUBMED	8306988				
REFERENCE	2 (bases 1 to 5156)				
AUTHORS	Valliy,J.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-JUL-1993) J. Valliy, Lab de Recherches Dermatologiques, Av De Valombrose Faculte de Medecine, 06107 Nice, Cedex 2, FRANCE				
COMMENT	Related sequence: Z15008.				
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	/chromosome="1"				
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BASE COUNT	1351 a 1222 c 1377 g 1206 t				
ORIGIN					
Query Match	74.1%; Score 2956.4; DB 9; Length 5156;				
Best Local Similarity	88.4%; Pred. No. 0;				
Matches 3285; Conservative	0; Mismatches 401; Indels 28; Gaps 6;				
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OY	199 TGCCGTGGCTTGCGTAGCTACTCTTCTCGCTCTCTCGCCGCGCGCACCGGG 258				

D	b		67	TGCCGCGCTGTGGCTGGGTGCCTGTCGACCCGCTGCTCCTCCTCCGAGCCGGG	126
O	y		259	CCACTCCGGGAGGGAAGTCTGTGATTGCAACGGGAATCCAAGCATATGATCTTTGACC	318
D	b		127	CCACTCCAGAGGGGAAAGTCTGTGTATTCATAAGGAAATCCAGGAGTGATCTTTGATC	186
O	y		319	AGGAACCTTCAAAACAGACAGAGAAATGGATTCCGCTGCCTCAACGTCANATGACAACATG	378
D	b		187	GGAACCTTCACAGACAAACTGTAATGATTCCTCGCTCAACTGCATATGACAACACTG	246
O	y		379	ATGGATCCACTGCGAGAGGTGCAGAAGCATTTTACCGACAGAGAAAAAGGACCGCT	438
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O	y		439	GTTTACCCCTGCAATTGTACTCTAAAGATCCTTAAAGCGTCGATGTGACAACTCTGGAC	498
D	b		307	TT	366
O	y		499	GGTGAGCTGTAAAGCCAGGTGTGACAGAGACAGGTGTGACCGATGTGTGCCGGCTCC	558
D	b		367	GGTGAGCTGTAAACCCAGGTGTGACAGGAGCAGATGGACCGATGTGTGCCAGGCTTCC	426
O	y		559	ACACACTACTGATGTGTTGGTGGCCGCCCAAAGCCAAAGCTCTGACTTCCAATGTACT	618
D	b		427	AATGTCTACCGAATGCGGGGTGCACCCAAAGCCACAGAGACTCTAGACTCCAAATGTACT	486
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D	b		487	GTGACCCAGCTGGGATCTCAGGGCCCTGTGACTACAGGGCCGTGTGTGTGCAAGCCGGCTG	546
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D	b		547	TCACTGTAGAGAGCGCTGTGATAGGTGTGACTACAGTTACTATTAATCTGATGGGGGAACC	606
O	y		739	CTCAGGCGTGAACCAAGTTTGTGTGTGTGGAACATCCGCCAGTCCCAAGCTCTGGGG	798
D	b		607	CTGAGGCGTGAACCAAGTTTGTGTGTGTGGAACATCCGCCAGTCCCGCAGCTCTGGAG	666
O	y		799	ACTACAGTGTCCATAAATCATCTCTGTGCTTCACATCAAGATGTGATGGCTGGAAGCGTG	858
D	b		667	AATACAGTGTCCATAAAGTACCTCTACCTTTCATCAAGATGTGATGGCTGGAAGCGTG	726
O	y		859	TCCAAAGAAACGGGTCTCTCTGCAAAAGCTCCAGTGTGTGACAGCGCCATCGGATATATTA	918
D	b		727	TCCAAAGAAAGGGTCTCTCTGCAAAAGCTCCAAATGGTCAACAGCCATCAAAATGTGTTA	786
O	y		919	GCTAGACGACGACGATCAACCCCTGTCTTATTTGTAGTCCGCAAAATTTCTTGGGAATC	978
D	b		787	GCTAGACCCCAAGACTAGACCCCTGTCTTATTTGTGTGCTCTGCGCCAAATTTCTTGGGAATC	846
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O	y		1039	ACCATATCGCCATAGAGTGTATCTCGGAAGGTGTGATCGATACGATCAACATCCCTGTA	1098
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O	y		1099	TGCCACTTGAACAGACACTGCTTGTGGGATACACCAAGACTTACACATTCAGATTTAATG	1158
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D	b		1087	GGAATTCACAGCCCTCGGATCCGAGTACTCTACGGAATATAGTACTGGATACATTTG	1146
O	y		1279	ACAAGGTGACTTGAATTTACAGCCCGCCGTTTCTGAGAGCCCAAGCGCCCTGGGTTGAC	1338



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OY 3244 GCAAGATGAACAGAGAGATGAGAGAGTGAAGTGTGGAAGAGAGAGAGAGAGAGAGAG 3303  
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OY 3304 CTTTGGCCATGAG 3363  
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[illegible]

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Best Local Similarity	88.7%	Pred. No. 0		
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DB 28	CGGATCCGCCATGCGCTGCGCTGTGGCTGCGCTGCTGCTCTGCTCTCTCTCTCTCC	87		
QY 248	CGCAGCCCGGGCCACCTCCGGGAGGGAAGTGTGTGATTGGCAACGGGAAGTCCAGGCATG	307		
DB 88	CGCAGCCCGGGCCACCTCCAGGAGGGAAGTGTGTGATTGGCAATGGGAAGTCCAGGCATG	147		
QY 308	CATCTTTGACGAGAACTTCAACAAACAGACAGAAATGGATTCCGCTCCCTCAACTGCA	367		
DB 148	TATCTTTGATGGGAACTTCAACAGAAACAGTGTATGGATTCCGCTCCCTCAACTGCA	207		
QY 368	TGACAACACTGATGGCATCCACTGCGAGAGGTGCAAGGCAAGATTTTACCGACAGAGA	427		
DB 208	TGACAACACTGATGGCATTTACTGCGAGAGAAGTGAAGAAATGGCTTTTACCGACAGAGA	267		
QY 428	AAGGAGCCGCTGTTTACCTGCAATGTATCTTAAAGTTCTCTTACGCTCGATGCA	487		
DB 268	AAGGAGCCGCTGTTTACCTGCAATGTATCTTAAAGTTCTCTTACGCTCGATGCA	327		
QY 488	CAACTCTGAGCGGTGACAGCTGTAAGCCAGGTGTGACAGAGACAGGTGACCGATGCT	547		
DB 328	CAACTCTGAGCGGTGACAGCTGTAAGCCAGGTGTGACAGAGACAGGTGACCGATGCT	387		
QY 548	GCCCGGCTTCCACACACTCACTGATGCTGGGTGCGCCAGACCAAGGCTGTAGACTC	607		
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QY 608	CAAGTGTGACTGTACACCGAGCTGGCATCTCAAGGCCCTCTGTACTACAGGCCCTGTGTG	667		
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QY	1328	CTGGGTTGAACAAATGTATATGCCCTGTGGCTGCAAGGGGCAAGTTCGCCAGATTTGTC	1387
Db	1168	CTGGGTTGAACAGTATATATGTCTGTTGGGTCAAAAGGGCAATTTCCAGAGATTTGTGC	1227
QY	1388	TTCCGGCTACAAAAGAAATTCAGCCAACTGGAACCTTTTGGCACCTGTATATCCATGTAA	1447
Db	1228	TTCTGGCTACAAAGAGAAATTCAGGGAACACTGGGGCCTTTTGGCACCTGTATATCTTGTAA	1287
QY	1448	CTGCCAAGGGGGAGGGGCGCTGCCATCCAGACACAGGAGACTGTATTCTAGGGGATGAAA	1507
Db	1288	CTGTCAAGGGGGAGGGGCGCTGTGTATCCAGACACAGGAGATGTATTATTCAGGGGATGAAA	1347
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
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 AUTHORS Boutaud, A.  
 JOURNAL Patent: WO 0066731-A 31 09-NOV-2000;  
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 EALSMSLAFVEYESTLKNRERFDLOVDRNKAERAKMRSLISTOKYSDASRPOOA  
 ERUGSNADNORAKNAGABALISSEIDELISLDEANVTADGLAMERGLASLKS  
 EMREVEGELEKLEFDTNMDAVQVITFAQRYDTAKNAGVTIQLTLDDLLHLM  
 DPLSVDEGLVLEOKLSRAKTOINSOLRPMSELEERRAORRHLHLETSIDEL  
 ADVKNLENINDNIPPCYNTQALQEQ"

BASE COUNT 959 a 862 c 1040 g 759 t  
 ORIGIN

Query Match 72.2%; Score 2880.8; DB 6; Length 3620;  
 Best Local Similarity 88.6%; Pred. No. 0;  
 Matches 3184; Conservative 0; Mismatches 387; Indels 21; Gaps 5;

QY 261 ACCTCGGAGGAGAGCTGTGATTCGACAGGGAAGTCAGGAATGATCTTGGACAG 320  
 Db 1 ACCTCGAGGAGGAGAGCTGTGATTCGACAGGGAAGTCAGGAATGATCTTGGATCGG 60  
 QY 321 GAATTCACAAACAGACAGGAATGATTCGCTGCTCAATGCAATGCAACACTGAT 380  
 Db 61 GAATTCACAGCAAACTGATATGATTCGCTGCTCAATGCAATGCAACACTGAT 120  
 QY 381 GGCATCCACTGCGAGAGGTGCAAGGCAATTTTACCAGACAGAGAAAGGACCGCTGT 440  
 Db 121 GGCATTCACACTGCGAGAGGTGCAAGGCAATTTTACCAGACAGAGAAAGGACCGCTGT 180  
 QY 441 TTACCCCTGCAATTTGATCTTAAGGTTCCTTAAGGCTGATGACAACTGTGACGG -500  
 Db 181 TTCCCTGCAATTTGATCTTAAGGTTCCTTAAGGCTGATGACAACTGTGACGG 240  
 QY 501 TGCAGCTGTAAAGCAGGTGTGACAGAGACAGGTGTGACAGATGTGCGCGCTTCAC 560  
 Db 241 TGCAGCTGTAAACAGAGGTGTGACAGAGACAGGTGTGACAGATGTGCGCGCTTCAC 300  
 QY 561 ACACTACAGTATGCTGGGTGCGCCCAAGCAAGCAAGCTGTAGATTCGAATGTGACTGT 620  
 Db 301 ATGCTACAGGATTCGGGGGTGACACCAAGCAAGCAAGCTGTAGATTCGAATGTGACTGT 360  
 QY 621 GACCCAGCTGATCTCAGAGGCTGCTGATGCTGAGCGCGCTGTGCAAGCGCGCTGTC 680  
 Db 361 GACCCAGCTGATCTCAGAGGCTGCTGATGCTGAGCGCGCGCTGTGCAAGCGCGCTGTC 420  
 QY 681 ACTGAGAGCGCTGTATAGTGTGACAGAGAGGTTACTATCACTGTGAGGGGAAACCT 740  
 Db 421 ACTGAGAGCGCTGTATAGTGTGACAGAGAGGTTACTATCACTGTGAGGGGAAACCT 480  
 QY 741 CAGGCTGTACCCAGAGTGTGCTATAGGCAATTCGCGCAGCTGCCAGACTGTGGGAC 800  
 Db 481 GAGGCTGTACCCAGAGTGTGCTATAGGCAATTCGCGCAGCTGCCAGACTGTGGGAA 540  
 QY 801 TACAGTGTCCATTAATATCATCTGCTGCTTCATCAAGATGTGATGAGTGAAGCTGTC 860  
 Db 541 TACAGTGTCCATTAATATCATCTGCTGCTTCATCAAGATGTGATGAGTGAAGCTGTC 600  
 QY 861 CAAAGAAAGCGGTCTCTGCAAGAGCTCCAGTGTGCAAGGCGCATCGGATATATTAGC 920  
 Db 601 CAAAGAAAGCGGTCTCTGCAAGAGCTCCAGTGTGCAAGGCGCATCGGATATATTAGC 660  
 QY 921 TCGACAGAGAGATCAACCTGTCTATTTGTAGTCTCTGCAAAATTTCTTGGAGTCAA 980  
 Db 661 TCGACAGAGAGATCAACCTGTCTATTTGTAGTCTCTGCAAAATTTCTTGGAGTCAA 720  
 QY 981 CAGGTAGCTATGCGAAAGCTGCTCTTGTGATACCGTGTGACAGAGAGGACAGACAC 1040  
 Db 721 CAGGTAGCTATGCGAAAGCTGCTCTTGTGATACCGTGTGACAGAGAGGACAGACAC 780  
 QY 1041 CCATTCGCCCATGATCTGATTCGGAAGGTGCTGATTCAGATTCACAGTCCCTTGATG 1100  
 Db 781 CCATTCGCCCATGATCTGATTCGGAAGGTGCTGATTCAGATTCACAGTCCCTTGATG 840  
 QY 1101 CCATTCGCAAGCACTGCTGTGTGGATTCACCAAGACTTACATTCAGATTAAATGAA 1160

[illegible]

Db	1915	CTTCAGGACATTTCTGAGAGATGCCACAGTTTTCAGAAAGTGGCTAGACAGATCCCTTGCTC	1974
Qy	2235	CGGGTGGCCAAAGCAGGACTCTCAAGAGAAATAGTACCGGGACCGCTGGATGATCCTCAAG	2294
Db	1975	CAGTTGGCCAAAGGTGAGGAGCCAAAGAGAAACGCTATCCAGAGCCGCTTGATGATCCTCAAG	2034
Qy	2235	ATGACTGTGGAAGAAGATTCCGGGCCCCCTGGGACGTCAGTATCGAAGCCAAAGTTTCAGATATCT	2354
Db	2035	ATGACTGTGGAAGAAGATTCCGGGCCCCCTGGGAGGTCAGTATCCAGAAACCGATTCGGGATATCT	2094
Qy	2355	CGCAGGCTCATCACTACATGATGCGCTTGAGCCCTGGAGGAAATGAGGGCTCCCTCGCAAAAC	2414
Db	2095	CACAGGCTCATCACTACATGATGAGCTTGAGCCCTGGCAGAAATGAAAGCTCTCTTGGGAAC	2154
Qy	2415	ACCAACATTCCTCTCTTCAGAGCAGTACCTAGGCGCCAAATGCTTTAAAGTCTGGCTCAG	2474
Db	2155	ACTAACATTCCTCTCTTCAGAGCAGTACCTAGGCGCCAAATGCTTTAAAGTCTGGCTCAG	2214
Qy	2475	GAGGCCACGAGATTGGCAGACAGCCATTTCAATCAGTACAGCCAGTAAATGAGCAACTGGCA	2534
Db	2215	GAGGCCACAAATTTAGCAGAAAGCCACGTTAGTACAGCCAGTAAATGAGCAACTGGCA	2274
Qy	2535	AAGGAAACCCGAGAGTATTTCCAAAGAGCTGATGATCTAGTGGGCGGAGGCTCTGCAGGAA	2594
Db	2275	AAGGAAACCTGAGAGTATTTCCAAACAGCCCTCTCACTAGTGGCGCAAGGCCCTGATTA	2334
Qy	2595	GGAG-----CCGGAAGCGGACAGCTTGAGCGAGGCGCGTGTCGAAAGGCTTGTGGGAAA	2648
Db	2335	GGAATCGGAAGCGGAAAGCGGTGATCCCGGACGGTGTGTGTGTGCAAGGGCTTGTGGAAAA	2394
Qy	2649	TTGCAGAAACTAAATCTGTGGCCAGAGTTGTGAGGAGGAGCCACGCAAAACGACATG	2708
Db	2395	TTGCAGAAACCAACATCTGTGGCCAGAGTTGACAAAGGAGGCGACATCAAGCGGAATTT	2454
Qy	2709	GAGCAGATAGGTCTTATCAGCATATGTTCCACCTTCTCAATTCCTGTCTCAATTTAG	2768
Db	2455	GAGCAGATAGGTCTTATCAGCACATGTTCCGCTCCCTGGATTCAGTGTCTCCGCTTAG	2514
Qy	2769	GGAGTCATGATCACTCTCTGGAGGT---AGAAAGGAGAGAGGCTAGACCAAAAGCTGAT	2825
Db	2515	GGAGTCATGATCACTCTCTGGAGGT---AGAAAGGAGAGAGGCTAGACCAAAAGCGAT	2574
Qy	2826	TCTCTCTCAAAACCGTGTGACTTAAGCATATGATGATGATTCAAAGCAGTGCAAAGCAATGTG	2885
Db	2575	TCATCTCTCAAGGCTGTGTAACACAGCATATGATGATGATTCAAAGCAGTGCAAAGCAATGTG	2634
Qy	2886	GGAACCTGGAGAGAAACCCGGCAGCTTTACAGAAATGGAAGATGGGAGACAGCA	2945
Db	2635	GGAACCTGGAGAGAAAGAACAGCAGCAGCTTTACAGAAATGGAAGATGGGAGAGAA	2694
Qy	2946	TCAGATCAGCTGCTTCCCGTGCACCAACTGGTAAACAGAGCCCAAGAAAGCACTAGT	3005
Db	2695	TCAGATCAGCTGCTTCCCGTGCACCAATTTGCTAAACAGAGCAACAAAGACACTGAT	2755
Qy	3006	ATGGGCAATGCCACTTTTATGAATTTGAGAAACATTTAAAGAAATCTCAGAGAGTTTGAC	3065
Db	2755	ATGGGCAATGCCACTTTTATGAATTTGAGAGCAATCTTAAAAACCTCAGAGAGTTTGAC	2814
Qy	3066	CTGCAGGTTGAGATTAAGAAAGCAGACAGCTGAAGAGGCCATGAGAGACTCTCTCAATCT	3122
Db	2815	CTGCAGGTTGAGCAACAGAAAGCCAGAACCTGAAAGAGCCATGAAAGACTCTCTCAATCT	2874
Qy	3126	AGCCAGAAAGTTGACAGGTGCCAGTGCATCAAGAGGAAGCAAGGCAAGAGCAGCCCTGGGAGT	3185
Db	2875	AGCCAGAAAGTTTTCAGATGCCAGTGCATCAAGAGCCAGCAAGCAAGAGAGCCCTGGGAGC	2933
Qy	3186	GCTGTGCCGAGCGCCACAGAGGCAAGAAATGACAGCCAGGAGAGCCCTGAGATCTGTGC	3245
Db	2935	GCTGTGCTGATGACACAGAGGCAAGAAATGGGCGCGGAGAGCCCTGGAATCTCAGT	2994
Qy	3246	AAGATAGAACAGAGATAGAGGTTGAACTTGAAGCCAAATGTGACAGCAGATGAGACC	3305
Db	2995	GAGATTTGAACAGAGATTTGGGAGTCTGAACTTGGAAAGCCAAATGTGACAGCAGATGAGACC	3054



OY	1101	CCACTGACGAAGACACTGCTTGTGGATGCACCAAGACTTAACATTCACTTACATTAAATGAA	1160
Db	841	CCACTTGGCAAGACACTGCTTGTGGCTCCACCAAGACTTAACATTCACTTAAATGAG	900
OY	1161	CATCCAAAGCAATATTGAGGCCCCAGCTAAGTACTTGAATGTGGAGGTTACTGCGG	1220
Db	901	CATCCAAAGCAATATTGAGGCCCCAGCTAGTACTTGAATGTGCAAGGTTAACTCGG	960
OY	1221	AACCTCAAGCCCTCGCGAATCCGAGCTACCTACGAGAAATACACTAGTGGGTACATTGAC	1280
Db	961	AATCTCAAGCCCTCCGAGTCCGAGCTAACATATGAGAAATACATACTGGGTACATTGAC	1020
OY	1281	AACGTGACCTTGAATTTACAGCCCCCGCTTCTTGAGCCCCAGCCCTGGGTTGAACAA	1340
Db	1021	AATGTGACCCCTGAATTTACAGCCCCCGCTCTCTTGAGCCCCAGCACCCCTGGGTTGAACAG	1080
OY	1341	TGTGTATGCCCCCTGTGGCTACAAAGGGGAGTTTCCAGAGATTTGGCTCCGGCTACAAA	1400
Db	1081	TGTATATGTCTCTGTGGGTACAAAGGGCAATTTCTCCACGAGATTTGCTTCTGGCTACAAAG	1140
OY	1401	AGAGATTCAGCCAGACTGGGACCTTTTGGACCTGTATTCCATGTAACTGCAAGGGGGA	1460
Db	1141	AGAGATTCAGGAGAACTGGGGCCCTTTTGGACCTGTATTCCTTGACTGCAAGGGGGA	1200
OY	1461	GGGGCCCTGGCATTCAGACACAGGAGAGCTGTACTCAAGGAGTGAAGAACCCGACATCCCT	1520
Db	1201	GGGGCCCTGTGTATCCAGACACAGGAGATTTGTATTACAGGGGATGGAATTCCTGCAAT--T	1257
OY	1521	GAGTGTGCTGACTGCCCATATGATGTTTTCACAAACATCCACAAAGACCCCGCAGCTGCAG	1580
Db	1258	GAGTGTGCTGACTGCCCAATTTGTTTTCACAAACATCCGACAGACCCCGCAGCTGCAG	1317
OY	1581	CCGTGGCCCTGTGCCAATGGGTTAGCTGCTCCCTGATGCTTGAGACAGAGAGAGTGGTG	1640
Db	1318	CCATGTCCCTGTCTAATACGGGGTTACAGCTGCTCACTGATTCGAGAGAGGAGAGAGTGGTG	1377
OY	1641	TGCATTAACCTGCCCCCAGGGGTGCTACTGATGCCCGTGTGACTGCTGCTGATGAGGCTAT	1700
Db	1378	TGCATTAACCTGCCCCCAGGGGTGCTACTGATGCCCGTGTGACTGCTGCTGATGAGGCTAT	1437
OY	1701	TTTGGGGACCCCTTGGGGGAACGTGGCCCACTGAGGCGCTTGTACGCCCTGTCACTGCAAC	1760
Db	1438	TTTGGGGACCCCTTGGGTGGAACATGAGGCCCACTGAGGCGCTTGTACGCCCTGTCACTGCAAC	1497
OY	1761	AACAAAGGAGCCCTAGTGGCTCCGGGGAACTGTACCGGCTGACAGGAGAGGTGTGAG	1820
Db	1498	AGCAATGTGGACCCCACTGCTCTTGGGAATTTGTACCGGCTGACAGGAGAGGTGTGAG	1557
OY	1821	TGCAATCCACAACACAGCTGGGGGTCCACTGTGACCAAGTGCANAAAGCAGGCTACTATGGGAC	1880
Db	1558	TGTATCCACAACAAGCCGCGCATCTACTGCGACAGTGCANAAAGCAGGCTACTTGGGGAC	1617
OY	1881	CCGTTGGCTCCCAATCCAGAGACAGAGTGTGACTTGCACACTGCACACCCAGTGGGCTCG	1940
Db	1618	CCATTTGGCTCCCAACCCAGAGACAGAGTGTGACTTGCACACTGCACACCCATGGGCTCA	1677
OY	1941	GAGCCTGTGAGTGTGCAAGTGTGAGCGACTGTGTGTTTGCACAGCCAGGCTTGTGGGCTCT	2000
Db	1678	GAGCCTGTGAGTGTGCAAGTGTGAGCGACTGTGTGTTTGCACAGCCAGGCTTGTGGGCCCC	1737
OY	2001	AGCTGTGAGCAATGCGGGCACTACCAAGCTGTCCAGCTTGTCTTAATCAAGTCAAGGTTACG	2060
Db	1738	AACGTGTGAGCAATGAGCAATT--CAGCTGTCCAGCTTGTCTTAATCAAGTCAAAATTCAG	1794
OY	2061	ATGATATCAGTTTATGACACAGCTCCAGATCCCTGGAGGGCCGATTTTGCAGAGCTACAGG-	2119
Db	1795	ATGATATCAGTTTATGACACAGCTTCCAGAGATGAGAGGCCCTGATTTCAAAGGCTCAGGGT	1854
OY	2120	-----TGGAGCAGTACCCACGACGAGCTGGAAGGACAGATGACGACGCTGAGCAGGCC	2174
Db	1855	GGTATGATGAGTATGATCCTGATACAGAGCTGTGAAAGGACAGATGACGACGCTGAGCAGGCC	1914

QY	2175	CTTGGGCACATTTCTGAGAGAAAGCCAGATTTTCACAAAGTGTGTTAAATCTCTTCAATCTC	2234
Db	1915	CTTCAGGACATTTCTGAGAGATGCCAAGATTTTCAAAGAGTGTCTACCAATCTCTTGCTCTC	1974
QY	2235	CGGGGGCCAAAGGCAAGGACACTCAAGAGATATGTACCGGGGACCGCTGGATGATCTCAAG	2294
Db	1975	CAGTTGGCCAAAGGTGAGAGGCCAAGACAGACGCTACCAAGAGCCCGCTGGATGATCTCAAG	2034
QY	2295	ATGACTGTGGAAGAGTTCCGGCCCTGGGGCAGTGTAGTATGAAAGCAAGTTTCAGATACT	2354
Db	2035	ATGACTGTGGAAGAGTTCCGGGCTCTGGGAAGTCAGTATCCAGAAACCAAGTTCCGGATACT	2094
QY	2355	CGCAGGCTCATCTACTCAGATGCGCCTGAGCCTGGAGAAAGTAGGCTTCCCTGCAAAAC	2414
Db	2095	CACAGGCTCATCTACTCAGATGACACTGAGCCTGGCAAAAGTAGAAGCTTCTCTGGGAAC	2154
QY	2415	ACCAACATTCCTCTCTCAGACACTACGTGGGGCCAAATGGCTTTAAAGCTTGCTCAG	2474
Db	2155	ACTAACATTCCTGCTCTCAGACCACTACGTGGGGCCAAATGGCTTTAAAGCTTGCTCAG	2214
QY	2475	GAGGCGACGAGATTGGCAGCAGCCATGTTAGTCACGCCAGTAACATGAGCAACTGCA	2534
Db	2215	GAGGCGACCAATATTAGCAGAAAGCCACGTTTAGTCAGCAGTAATACATGAGCAACTGACA	2274
QY	2535	AAGGAACCCAGAGATATTCCAAAGAGCTGATGTCTACTGTTGGCGGAGGCTCTGCAAGAA	2594
Db	2275	AGGGAAGATGAGACTATTTCCAAACAGCCCTCTACACTGGTGGCCAGGCCCTCATGAA	2334
QY	2595	GGAG-----GCGGAAGCGGCACGCTGGACGAGACCCTGGTGCAAAAGCTTTGGGAAAA	2648
Db	2335	GGAGTCGGAAACGGGAAGCGATGAGCCGAGACGCTCTGTGGTGCAAGGGCTTTGGAAAA	2394
QY	2649	TTGCAGAAACCTAAATCTCTGGCCAGAGATGTTCGAGAGGGAGGCACAGCAACCGCATG	2708
Db	2395	TTGGAAGAAACCAAGTCCCTGGCCACAGAGTGTGACAAAGGAGGCCACTCAAGCGGAATT	2454
QY	2709	GAAGCAGATAGGTCTTATCAGCATATGTCCTCACCTTCTCAATTCCTGTTCTCAGATTGAG	2768
Db	2455	GAAGCAGATAGGTCTTATCAGCACACAGTCTCCGCTCTGGATTCAGTGTCCGCTTCAG	2514
QY	2769	GGAGTCATGTATCAGTCTCTTGCAGT---AGAACGAAAGAGGCTCAGACAAAAAGCTGAT	2825
Db	2515	GGAGTCAGTGTATCAGTCTCTTCAAGGTGAAAGCAAGAGATCAAAACAAAAAGCGAT	2574
QY	2826	TCTCTCTAAACCGGTGACTTAAGCATATGATGATGATGTTCAAGCACTGACAAAGCAATCTG	2885
Db	2575	TCACTCTTAACCTGTGTACCAAGCATATGTGATGTGATTCAAGCGCTACACAAAGAAATCTG	2634
QY	2886	GGAACCTGGGAAGAAAGAACCCGGCAGCTCTTACAGATGGAAGAAATGGGAGACAGACA	2945
Db	2635	GGAACCTGGAAAGAAAGAACGACAGAGCTCTTACAGATGGAAGAAATGGGAGAGAGAA	2694
QY	2946	TCAGATCAGTGTCTTCCCGTGGCAACCTTCTTAAAGCAGAGCCCAAGAAAGCACTAAGT	3005
Db	2695	TCAGATCAGTGTCTTCCCGTGGCAACCTTCTTAAAGCAGAGCAACAAAGAAAGCACTGAGT	2754
QY	3006	ATGGGCAATGGCACTTTTATGAAGTTGAGAACAATCTTAAAGATCTCAGAGAGTTGAC	3065
Db	2755	ATGGGCAATGGCACTTTTATGAAGTTGAGAGCAATCTTAAAGATCTCAGAGAGTTGAC	2814
QY	3066	CTGCAGGTGGAGATTAAGAAAGACAGAAAGCTTAAGAGGCCATGAAGAGACTCTCTACATC	3125
Db	2815	CTGCAGGTGGAGAACAGAAAGACAGAAAGCTTAAGAGGCCATGAAGAGACTCTCTACATC	2874
QY	3126	AGCCAGAAAGTTTGACAGTGGCCAGTGACAAAGCAAGACAGCAAGCAAGCAAGCCCTGGCAGT	3185
Db	2875	AGCCAGAAAGTTTTCAGATGGCCAGTGACAAAGCAAGACAGCAAGCAAGCAAGCCCTGGGAGC	2934
QY	3186	GCTGTGTGCCAGCGCCAGAGGGCAAAAGATGCACAGGAGAGGCCCTGGAGATCTGTGGC	3245
Db	2935	GCTGTGTGTATGCAACAGAGGCAAAAGATGGGGCGGGGAGGCCCTGGAATCTCAGT	2994
QY	3246	AAGATAGAACAGGAGATATGAGAGGTCGTGAATCTTGGAAAGCAATGTGACAGCATGAGAGCC	3305



Db	2995	GAGATTGAACAGACAGATTGCGAGTCTGAACTTGGAAAGCCAAATGTGCACAGCATGTGAGACC	3055
QY	3306	TTGGCCATTGAGAGAGGAGCTGGCCACTCTGAAAAGTGAGATGAGAGAGTGGAGAGAG	3365
Db	3055	TTGGCCATTGAGAAAAGAGACTGGCTCTCTCTGAAAGACTGAGATGAGGAAAGTGGAGAGAG	3115
QY	3366	CTGTCAAGGAAGACAGAGAGCTTTTACATGGATATGAGACGAGTGCAGATGGTAATTGCA	3422
Db	3115	CTGGAAGGAAGAGAGACTGAGAGTTTATGACAGGAATATGAGATGAGTGCAGATGGTGTACAA	3175
QY	3426	GAGGCCCCAAAGAGTTGAAAAACAGAGCCCAAGAAATGCTGGAGTTAGCATCCAAAGACACTTC	3485
Db	3175	GAGGCCCAAGAGGTTGATATCCAGAGCCCAAGAAAGCTGGGGTTTACATTCAMAGCACACTC	3235
QY	3486	AACACATTGGATGGCATCTTACACCTAAATAGACCAGCCCTGGCAGTGTGGATGAAAGAGAG	3545
Db	3235	AACACATTAGACGGGCTCTCTGATGTGATGAGACAGCCCTCTCAGTGTGATGATGAAAGAGG	3295
QY	3546	CTGATCTTACTGAGACAGAGCTTTTCCGAGCCAAAGACTCAGATCAAGACCCAGCTACGG	3605
Db	3295	CTGGTCTTACTGAGACAGAGCTTTCGAGGCCAAGACCAGATCAAGCCAACTGGCG	3355
QY	3606	CCCTTGATGTGAGCTGTGAGAGAGAGGGGACACATCGGCAGAAAGGCCACTCTCGTTCTGT	3665
Db	3355	CCCATGATGTGAGACTGTGAAGAGAGGGGACGCTGACAGAGAGGGGCACTCTCATTTGGCTG	3415
QY	3666	GAGACTAGCATGATGAGGATTTCTGGCTATGTGAGAGACCTGGAGACATCGAGGACAAAC	3722
Db	3415	GAGAACACATGATGATGGGATTTCTGGCTATGTGAGAAACTTGTGAGAACATTTAGGACAAAC	3475
QY	3726	CTGCCCCGGGCTGCTACAAATACCCAGGCTCTTGAGCAACAGTGAAGCTGCTTAGAGAT	3785
Db	3475	CTGCCCCCAGGCTGCTACAAATACCCAGGCTCTTGAGCAACAGTGAAGCTGCCATTAAATAT	3535
QY	3786	TTCTCAACCAAGGTTCTTGGGATTCAGACGTACAGTCCCTTAGAGATTTCTCA	3837
Db	3535	TTCTCAACTGAGGTTCTTGGGATTCAGATCTCAGGGCTCGGAGGCATGCTCA	3586
RESULT 9			
LOCUS	162750	4316 bp	DNA linear PAT 07-OCT-1997
DEFINITION	Sequence 14 from patent US 5660982.		
ACCESSION	162750		
VERSION	162750.1	GI:2480458	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 4316)		
TITLE	Trygvason,K., Kallunki,P. and Pyke,C.		
JOURNAL	laminin chains: diagnostic uses		
FEATURES	Patent: US 5660982-A 14 26-AUG-1997; Location/Qualifiers 1..4316		
BASE COUNT	1158 a 1033 c 1226 g 899 t		
ORIGIN	/organism="unknown"		
Query Match	68.3%; Score 2726; DB 6; Length 4316;		
Best Local Similarity	88.5%; Pred. No. 0;		
Matches 3045; Conservative 0; Mismatches 365; Indels 30; Gaps 7;			
QY	99	AAGGAAAAGGAAGCAGACAGCGGAGCGCAGATGAGAACTCCACAGCGGCGAGAGCCCGGGC	158
Db	14	AAGGAAAAGGAAGCAGACAGCGGAGCGCAGAGTTGAAACACACAAAC--CGAGGCGCGGGC	71
QY	159	AGCAGCCCTGACAGCGCG-----GACCAGCGGCGGCGCTGGGAGTGCCTGGGCTGTG	211
Db	72	AGCAGCCCTGACAGCGGAGAGACAGACTGAGAGCGGCGCGCACCGCCATGCTGGGCTGTG	131
QY	212	GCTAGGCTGCTACTCTGCTTCTGCGCTCTCTCTGCGCGGACCGCGGCGCACTCCGGAG	271

Db	132	GGTGGGCTGCTCCCTCTGCTTCTGCTCTCTGCTGCGGAGCCGGGCGACCTCCAGGAG	191
Qy	272	GGAACTCTGTGATTCACACGGAGATTCAGGCAATGCATCTTTGACAGAACTTCACAA	331
Db	192	GGAACTCTGTGATTCACAAATGGGAACTCCAGGCAAGTATCTTTGATTCGGGAACTTCACAG	251
Qy	332	ACAGACAGGAATGGAATTCGCTGCCCTCACTGCAATGACAACTGATGATGCATCCACTG	391
Db	252	ACAAACTGGTAAATGGATTCGCTGCCCTCAAACTGCATGACAACTGATGATGCATTCCTG	311
Qy	392	CGAGAGGTGACAGGACGAGATTTTACCAGACAGAGAAAGGAGCGGCTCTTAACCTCGCA	451
Db	312	CGAGAGGTGACAGGAATGGCTTTTACCGGACACGAGAAAGGAGCCGCTGTTTGCCTGCA	371
Qy	452	TTGTAACTCTAAAGGTTCTCTTAGCGCTCGATGTACAACTCTTGACGGTGCAGCTGTAA	511
Db	372	TTGTAACTCTCAAAAGTTCTCTTAGTGCTCGATGTACAACTCTTGACGGTGCAGCTGTAA	431
Qy	512	GCCAGGTGTACAGAGACAGAGTGTGACCGATGTCTGCCCGGCTTCCACACACTCACGA	571
Db	432	ACCAGGTGTGACAGAGACAGATGCGACCGATGTCTGCCCGGCTTCCACATGCTCACGA	491
Qy	572	TGCTGGGTGCGCCCAAGACCAAGGCTGCTAGACTTCGAATGTGACTGTGACCCAGCTGG	631
Db	492	TGCGGGGTGACCCCAAGACACAGAGACTGCTAGACTTCGAATGTGACTGTGACCCAGCTGG	551
Qy	632	CATCTCAGGGCCCTGTGACTCGCGCGGTGTGCAAGCGCGGTGACTGACGTGAGAGG	691
Db	552	CATCTCAGGGCCCTGTGACTCGCGCGGTGTGCTGCAAGCGCGGTGACTGACGTGAGAGG	611
Qy	692	CTGTGATAGGTGACACAGGTTACTATCACCTGATGGGGAAACCTTCAGGGGCTGTAC	751
Db	612	CTGTGATAGGTGATCAGATGATTACTATTAATCTGATGGGGGAAACCTTCAGGGGCTGTAC	671
Qy	752	CCAGTGTGTTTGTCTATGCGCAATTCGCCAGCTGCCACAGCTCTGGGGACTTACAGTGTCA	811
Db	672	CCAGTGTGTTTGTCTATGCGCAATTCAGCGAGCTGCCAGCTCTGCGAATACAGTGTCA	731
Qy	812	TAAATATCAATCTGCTTCATCAAGATGTTGATGGCGGAAAGGCTGCCAAAGAAAGG	871
Db	732	TAAATATCAATCTTACCTTCATCAAGATGTTGATGGCGGAAAGGCTGCCAAAGAAAGG	791
Qy	872	GTCCTCTCCAAAGCTCCAGTGGTGCACAGCGGCATGGGATATTTAGCTCAGCAGCAG	931
Db	792	GTCCTCTCCAAAGCTCCCAATGGTGCACAGCGGCATCAAGATGTTTACTCAGGCCAAC	851
Qy	932	ATCAGACCCCTGTATTTTGTAGCTCTGCGCAAAATTTTGGGAATCAACAGGTGAGCTA	991
Db	852	ACTAATATCTGTCTATTTTGTAGCTCTGCGCAAAATTTTGGGAATCAACAGGTGAGCTA	911
Qy	992	CGGGGAAAGCCATCTTTTGAATACCGGTGGATGGGGGAGGAGACACCCATCTGGCCA	1051
Db	912	TGGGGAAGCCGTGCTTTTGAATACCGGTGGAGAGGAGGAGACACCCATCTGGCCA	971
Qy	1052	TGACCTGATCTCGAAGGTGCTGTGCTACAGGATCAGACCTCCCTTGATGACCATTCAGCA	1111
Db	972	TGATGTATCTCGAAGGTGCTGTGCTACAGGATCAGACCTCCCTTGATGACCATTCAGCA	1031
Qy	1112	GACACTGCTTTGTGGATCACCAAGCTTACACATTCAGATTTAAATGAATCCAGCAG	1171
Db	1032	GACACTGCTTTGTGGGCTCACCAAGACTTACACATTCAGGTTAAATGAGACTCCAGCA	1091
Qy	1172	TAAATGAGGCCCCCAGCTAAATTTACTTGAATTCGAGGTTTACTGCGGAGACTTCACGC	1231
Db	1092	TAAATGAGGCCCCCAGCTGAGTTTACTTGAATTCGAGGTTTACTGCGGAGACTTCACGC	1151
Qy	1232	CCTGGAGATCCGAGCTACCTACGAGGAATACAGTACTGGGTACATTGCAACGTGACCTT	1291
Db	1152	CCTCGGATCCGAGCTACATATGGAAGATACAGTACTGGGTACATTCGCAATGTGACCTT	1211
Qy	1292	GATTTTCAAGCCGCGCGTCTCTGAGGCCACGCGCGCTGGGTTGAACATGTGATGCCC	1351









Df		3246	AAAGGACGTGGCCTCTCTGGAAGAGATGAGATGAGGAAGTGGAAAGGAGAGCGTCGAAAAGGA	3305
OY		3377	GGAGCAGAGAATTGCATGATGATATGAGACCCACTGCATGCTAATGTGACAGAGCCCCAAG	3438
Df		3306	GGAGCTGGAGTTTGACACAGAAATATGGAAGCAGTACAGATGCTGATTTACAGAGGCCAGAA	3365
OY		3437	AGTTGAAACAGAGAGCAAGTAATGCTGGAGTTACGATCCACAGACACATCAACATATGGA	3496
Df		3366	GGTGTGATACCAGAGCCAGAACCGCTGGGGGTTACATCCACAACACTCAACACTTATGA	3425
OY		3497	TGGCATCTCTACACCTAATAAG	3516
Df		3426	CGGCCTCTGCATCTGATGG	3445
RESULT 11				
MNU43327				
LOCUS		MNU43327	5158 bp	mRNA linear ROD 26-FEB-2002
DEFINITION		Mus musculus lamlnln gamma 2 chain precursor (B2t) mRNA, complete cds.		
ACCESSION		U43327	S75987	
VERSION		U43327.2	GI:18921413	
KEYWORDS		.		
SOURCE		Mus musculus.		
ORGANISM		Mus musculus.		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS		1 (bases 1 to 5158)		
TITLE		Yamada,Y.		
JOURNAL		Direct Submission		
REFERENCE		Submitted (13-DEC-1995) Laboratory of Developmental Biology,		
AUTHORS		National Institute of Dental Research, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA		
TITLE		2 (bases 1 to 5158)		
JOURNAL		Sugiyama,S., Utani,A., Yamada,S., Kozak,C.A. and Yamada,Y.		
AUTHORS		Cloning and expression of the mouse laminin gamma 2 (B2t) chain, a		
TITLE		subunit of epithelial cell laminin		
JOURNAL		Eur. J. Biochem. 228 (1), 120-128 (1995)		
MEDLINE		95188894		
PUBMED		7882992		
REFERENCE		3 (bases 1 to 5158)		
AUTHORS		Sasaki,T., Gohring,W., Mann,K., Brakebusch,C., Yamada,Y., Fassler,R. and Timpl,R.		
TITLE		Short arm region of laminin-5 gamma2 chain: structure, mechanism of processing and binding to heparin and proteins		
JOURNAL		J. Mol. Biol. 314 (4), 751-763 (2001)		
MEDLINE		21592560		
PUBMED		11733994		
REFERENCE		4 (bases 1 to 5158)		
AUTHORS		Sasaki,T. and Yamada,Y.		
TITLE		Direct Submission		
JOURNAL		Submitted (26-FEB-2002) Laboratory of Developmental Biology,		
REFERENCE		National Institute of Dental Research, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA		
COMMENT		Sequence update by submitter		
REMARK		On Feb 26, 2002 this sequence version replaced gi:1151216.		
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[illegible]

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Oy	2409	CAAAAACCAACATtTCTCTCTTACAGAGCACTACGTGGGGCCAAATGGCTTtTAAAGTCTG	2468
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Dp	2518	GGAGTCAAGTATCTGTCTCTTTCAGGTGGAACAAAGAGATCAAGACAAAAAGGCTGATtCT	2577
Oy	2829	CTCTCAAACCGTGTGACTTAAGCATATGTGATGAGTtTCAAGCAGGTGCAAAGCAATCTGGGA	2888

Db	2578	CTCTAAACCTGCTGATCCAGACAAACCGATGCATTACGCGCTGTCGAAACAATCTG66G	2637
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Db	2638	AACCTGGGAAGAAACCGGAGCTTTTACAGACTGGAAAGATGAGACAGACTTCA	2697
QY	2949	GATCAGCTGCTTCCCGTCCCAACCTTGCTTAAAGCACAAGCCCAAGAGCACTAATG	3008
Db	2698	GATCAGCTGCTTCCCGTCCCAACCTTGCTTAAAGCACAAGCCCAAGAGCACTAATG	2755
QY	3009	GGCAATGCCACTTTTATGAAGTTGAGAAATCTTAAAGATCTCAGAGCTTGACCTG	3068
Db	2758	GGCAATGCCACTTTTATGAAGTTGAGAAATCTTAAAGATCTCAGAGCTTGACCTG	2817
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QY	3789	TCAAC	3793
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RESULT 14

MUSNIC

LOCUS

DEFINITION

ACCENSION

VERSION

MUSNIC

Mus musculus

1393 bp

100kda nIc6in (Nl6B2)

GI:833765

mRNA

Linear

sequence.

ROD 08-JUN-1995

KEYWORDS	laminin; nicein.
SOURCE	Mus musculus strain C57BL/C CDNA to mRNA.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 1393)
TITLE	Aberdam,D., Galliano,M.F., Mattei,M.G., Pisanì-Spadafora,A.,
JOURNAL	Ortonne,J.P. and Meneguzzi,G.
MEDLINE	Assignment of mouse nicein genes to chromosomes 1 and 18
PUBMED	Mamm. Genome 5 (4), 229-233 (1994)
AUTHORS	94281750
TITLE	8012114
JOURNAL	2 (bases 1 to 1393)
MEDLINE	Aberdam,D., Aguzzi,A., Baudoin,C., Galliano,M.F., Ortonne,J.P. and
PUBMED	Meneguzzi,G.
AUTHORS	Developmental expression of nicein adhesion protein (laminin-5)
TITLE	subunits suggests multiple morphogenic roles
JOURNAL	Cell Adhes. Commun. 2 (2), 115-129 (1994).
MEDLINE	94363405
PUBMED	8081888
REFERENCE	3 (bases 1 to 1393)
AUTHORS	Aberdam,D.
TITLE	Direct Submission
JOURNAL	Submitted (02-MAY-1994) Daniel Aberdam, Faculte de Medecine, INSERM
MEDLINE	U385, Ave de Valombrose 06107, Nice Cedex 2, France
PUBMED	On May 26, 1995 this sequence version replaced gl:476722.
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Phasianinae; Gallus.  
REFERENCE  
AUTHORS  
TITLE  
1 (bases 1 to 3020)  
Halfier,W., Dong,S., Balasubramani,M. and Bier,M.E.  
Absent histogenesis after temporary disruption of the retinal  
basal lamina  
JOURNAL  
Unpublished  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
2 (bases 1 to 3020)  
Dong,S., Balasubramani,M., Halfier,W. and Bier,M.E.  
Direct Submission  
Submitted (26-APR-2001) Neurobiology, University of Pittsburgh,  
3500 Terrace Street, Pittsburgh, PA 15261, USA

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BASE COUNT 693 a 855 c 912 g 560 t  
ORIGIN

Query Match 13.2%; Score 528.2; DB 5; Length 3020;  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 02:13:43 ; Search time 801 Seconds  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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No.	Score					
1	2986.2	74.9	5200	17	AAT13323	Kallinin/Laminin 5
2	2986.2	74.9	5200	21	AAC83729	Human laminin 5
3	2986.2	74.9	5200	24	AAL42910	Laminin gamma-2 ch
4	2956.4	74.1	5156	21	AAC65866	Human lung cancer-
5	2956.4	74.1	5156	24	ABL49085	Human lung tumor
6	2944.2	73.8	3720	21	AAC83731	Human laminin 5 cd
7	2908.4	72.9	5152	20	AAZ24627	Human lung tumor a
8	2804	72.8	3582	24	AAD31145	Human laminin gamm
9	2880.8	72.2	3620	21	AAC83732	Human laminin 5 cd

10	2879.2	72.2	5020	21	AAC83730	Human laminin 5 cd
11	2726	68.3	4316	17	AAT13324	Kallinin/Laminin 5
12	2726	68.3	4316	24	AAL42911	Laminin gamma-2 ch
13	2590	64.9	5159	21	AAC83733	Mouse laminin 5 cd
14	2567.8	64.4	3579	24	AAD31144	Mouse laminin gamm
15	2537.4	63.6	5057	21	AAC83734	Mouse laminin 5 cd
16	515.6	12.9	4948	21	AAAB8902	Human laminin 2 ga
17	515.6	12.9	4948	21	AAC83712	Human laminin 8 cd
18	515.6	12.9	4948	24	ABO72913	Human laminin 10 t
19	515.6	12.9	4972	21	AAAB8904	Human laminin 2 ga
20	515.6	12.9	5306	21	AAAB8901	Human laminin 2 ga
21	515.6	12.9	5306	21	AAC83713	Human laminin 8 cd
22	515.6	12.9	5306	24	ABO72912	Human laminin 10 t
23	515.6	12.9	5330	21	AAAB8903	Human laminin 2 ga
24	515.6	12.9	7263	24	ABK09760	Human ovarian tumo
25	514.6	12.9	7263	21	AAAB8906	Mouse laminin 2 ga
26	514.6	12.9	7263	21	AAC83716	Mouse laminin 8 cd
27	514.6	12.9	7263	24	ABO72915	Mouse laminin 10 t
28	514.6	12.9	7554	21	AAAB8905	Mouse laminin 2 ga
29	514.6	12.9	7554	21	AAC83715	Mouse laminin 8 cd
30	514.6	12.9	7554	24	ABO72914	Mouse laminin 10 t
31	514.6	12.9	8145	22	AAT26595	Human breast cancer
32	410.4	10.3	603	21	AAZ80498	Human colon cancer
33	388	9.7	551	21	AAZ80364	Human colon cancer
34	381.8	9.6	742	20	AAK98755	Human validated ca
35	366.8	9.2	551	22	AAK47190	Human breast cancer
36	366.8	9.2	551	22	AAK1760	Human breast cancer
37	350.2	8.8	3540	24	AAT10820	Mouse laminin-15 g
38	350.2	8.8	4890	20	AAC9766	CDNA encoding huma
39	350.2	8.8	5300	21	AAC75126	Human ORFX ORF61
40	345.4	8.7	560	24	ABO58183	Human colon cancer
41	287.4	7.2	5703	23	ABL05981	Drosophila melanog
42	265.2	6.6	1778	24	ABL67677	Oesophagus cancer
43	231.8	5.8	8927	23	ABL05980	Drosophila melanog
44	211.2	5.3	419	21	AAC03416	Human secreted pro
45	170.6	4.3	193	24	ABK29643	Colon adenocarcino

## ALIGNMENTS

RESULT 1  
AAT13323  
ID AAT13323 standard; CDNA: 5200 BP.  
AC AAT13323;  
XX  
DT 13-NOV-1996 (first entry)  
XX  
AC  
DE Kallinin/Laminin 5 gamma-2 chain coding sequence.  
XX  
KW Kallinin: laminin; epidermolysis bullosa; junctional; probe;  
XX detection; inhibit; monitor; malignancy; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
XX Key location/Qualifiers  
XX CDS 118..3699  
XX FT /\*tag= a  
XX FT /product= kallinin/laminin-5-gamma-2-chain  
XX PD  
XX W09610646-A1.  
XX  
XX 11-APR-1996.  
XX  
XX 04-OCT-1995; 95WO-EP03918.  
XX  
XX 04-OCT-1994; 94US-0317450.  
XX  
XX (TRYG/) TRYGVASON K.  
XX  
XX Kallunki P, Pyke C, Trygvason K;  
XX  
XX

DR	WPI: 1996-209366/21.
DR	P-PsDB; AAR91427.
XX	Detection of kalinin or lamnin 5 expression in cells - useful to
PT	detect, monitor and inhibit the invasive growth of cell in tissue,
PT	partic. malignant tissue
XX	
PS	Disclosure: Fig 4A; 37pp; English.
CC	
CC	The present sequence is the full cDNA (Genbank Z15008) encoding the
CC	kalinin/laminin 5 gamma-2 chain (R91427). The gamma-2 chain is of
CC	importance to patients suffering from epidermolysis bullosa, esp. the
CC	junctional form (JEB). Probes and antisense gamma-2 sequences derived
CC	from this sequence can be used to detect, monitor and inhibit the
CC	invasive growth of cells in tissue, partic. malignant tissue.
XX	
SQ	Sequence 5200 BP; 1364 A; 1236 C; 1392 G; 1208 T; 0 other;
Query Match	74.9%; Score 2986.2; DB 17; Length 5200;
Best Local Similarity	88.5%; Pred. No. 0;
Matches 3328:	Conservative 0; Mismatches 403; Indels 30; Gaps 7
OY	99 AAGGAAAAGGAAGCAGACAGCGAGCGGCAAGTGTAGAATCTCCAGCGGGCGCGCGGC 158
Db	14 AAGGAAAAGGAAGCAGACAGCGGAGCGGCAAGTGTAGAAACCACCAAC--GAGCGCGCGGC 71
OY	159 AGCGACCCCTGACGCGCG-----GACCGCGCGCGCGCTTGCCATGCTCGCTCTG 211
Db	72 AGCGACCCCTGACGCGGAGACAGACTGAGCGCGCGCGCACCGCATGCTGCGCTCTG 131
OY	212 GCTGAGCTGTACCTCTGCTCTGCTCTCTGCGCGAGCGCGGCGGCGACTCCGGAG 271
Db	132 GCTGAGCTGTGCT 191
OY	272 GGAAGTCGTATTGCAACGGGGAATCCAGGCATCATCTTTGACAGAACTTCACA 331
Db	192 GGAAGTCGTATTGCAATGGGAATCCAGGCAAGTATCTTTGATCGGAACTTCACAG 251
OY	332 ACAGACAGGAANTGGATTCGCTGCTGCTCACTGCAATGACACAACTGATGGCATCACTG 391
Db	252 ACAAACTGCTATGATGATTCGCTGCTCACTGCAATGACAACTGATGGCATCACTG 311
OY	392 CGAGAGGTGCAAGGAGGATTTTACCGACAGAGAAAGGAGACCGCTTTTAACCTGCAA 451
Db	312 CGAGAGGTGCAAGGAATGGCTTTTACCGGACAGAGAAAGGAGACCGCTTTTGGCCTGCAA 371
OY	452 TTGTAACTCTAAAGGTTCTTTAGCGCTGCATGTGACAACTCTGGACGGTGCAGCTGTA 511
Db	372 TTGTAACTCCAAGGTTCTTTAGGCTGCATGTGACAACTCTGGACGGTGCAGCTGTA 431
OY	512 GCCAGGTGTGACAGGAGACAGGTGTGACCGATGTCTGCCGCGTTCCACACACTCATGA 571
Db	432 ACCAGGTGTGACAGGAGACAGATGTGACCGATGTCTGCCAGGCTTCCACATGTCTACGGA 491
OY	572 TGCTGGGGGCCCCCAAGAACCAAGGCTCTAGACTCCAAAGTGTACTGTGACCCAGCTGG 631
Db	492 TGCGGGGGTGCACCCAAAGACAGAACTGTGACTCAACTCAAGTGTGACTGTGACCCAGCTGG 551
OY	632 CATCTCAAGGGCCCTGTGACTCAGGCGGCTGTGCTGCAAGCGCGGCTGTCACTGGGAGCG 691
Db	552 CATGCGAGGGCCCTGTGACGCGGCGGCTGTGTCTGCAAGCCAGCTGTTAATCGGAGAACG 611
OY	692 CTGTGATAGGTGTGCAACCAAGTACTATCACTGGATGGGGGAAACCTTCAGGGCTGTAC 751
Db	612 CTGTGATAGGTGTGATCAGTACTATAACTGTGATGGGGGAAACCTTCAGGGGCTGTAC 671
OY	752 CCAAGTTTTTGTGCTATGGGCAATTCGCCAGCTGCCACAGCTGTGGGCACTACAGTGTCCA 811
Db	672 CCAAGTTTTTGTGCTATGGGCAATTCAGCAGCTGCCGAGCTGTGAGAAATACAGTGTCCA 731
OY	812 TAAATATATCTCTGCTTCATCAAGATGTTGATGGCGGAAAGGCTGTCCAAAGAAAGG 871
Db	732 TAAATATACCTCTACCTTTCATCAAGATGTTGATGGCGGAAAGGCTGTCCAAAGAAATGG 791

QY	872	SMCTCTGCAAAAGCCCGATGGGTGACACAGCGCATCGGGATATATTGAGTCACAGCAG	931
Db	792	GTCTCTGCAAAAGCTCCATGATGACACAGCGCATCAAGATGTGTTAGCTGACCCAAAG	851
QY	932	ATCAGACCCCTCTATTTTGTAGTCCTCGCCAAATTTCTTGGGAAATCAACAGTGACTA	991
Db	852	ACTAGATCTCTGTATATTTTGTGGGCTCGCCAAATTTCTTGGGAAATCAACAGTGACTA	911
QY	992	CGGGCAAAAGCCTATCTTTTGAACACCGTGTGGATAGGGGAGGACAGACCCATCTGCCA	1051
Db	912	TGGGCAAAAGCCGTCTCTTTTGAACACCGGTGTGGAGAGGAGGACAGACCCATCTGCCA	971
QY	1052	TGAGCTGATCCGGAAGGTGCGGGGCTACGGATCAACAGCTCCCTGATGGCCACTTAGCA	1111
Db	972	TGATGTGATCTCGGAAGGTGCTGGGCTACGGATCAACAGCTCCCTGATGGCCACTTAGCA	1031
QY	1112	GACACTGECCTGTGGGATCACCAGACCTTACATTCGATTAAATGAAATCCCAACAG	1171
Db	1032	GACACTGECCTGTGGGCTCACCAGACCTTACATTCGATTAAATGAAATCCCAACAG	1091
QY	1172	TAAATGGAGCCCCCAGCTTAAGTTACTTGAATATCGGAGGTTACTGGGAAACCTCACAGC	1231
Db	1092	TAAATGGAGCCCCCAGCTGAGTTACTTGAATATCGAAGGTTACTGGGAAATCCACAGC	1151
QY	1232	CCTGGGATCCGAGCTACCTACGGAATACAGTACTGGGATGATTCGAAACGTGACCTT	1291
Db	1152	CCTGGGATCCGAGCTACATATATGAGAAATACAGTACTGGGATGATTCGAAATGTGACCT	1211
QY	1292	GATTTACAGCCGCCCGCTTCTGTGAGCCCGCCCGCTGGGTTGAACATGTGATGCC	1351
Db	1212	GATTTACAGCCCGCCTGTCTGTGGAGCCCGCCAGCACCCGCGGGTTGAACATGTGATGCC	1271
QY	1352	TGTTGGCTACAAAGGGGCGATTCTCGACAGATGTGGCTTCGGGCTACAAAGAGATTCAGC	1411
Db	1272	TGTTGGGATCAAGGGGCAATTCCTCGACAGATGTGGCTTCGGCTACAAAGAGATTCAGC	1331
QY	1412	CAGACTGGGACCTTTTGGCACCTGATTCATTCATGTAACCTGCCAAGGGGAGGGGCTCGA	1471
Db	1332	GAGACTGGGGGCTTTTGGCACCTGATTCATTCATGTAACCTGCCAAGGGGAGGGGCTCGA	1391
QY	1472	TCACAGACACAGAGAGACTGTACTAGAGGGGATGAGAACCTTGACATCCCTGAGTGTCTGA	1531
Db	1392	TCACAGACACAGAGAGATGTGTATTACAGGGGATGAGAAATCTGTGACAT ---TGAGTGTCTGA	1448
QY	1532	CTGGCCCCATGGTTTCTACACAGATCCACAGACCCCGGACGCTGCCAAGCCGTGCCCTG	1591
Db	1449	CTGCCAATGTGTTTCTACACAGATCCGACAGACCCCGGACGCTGCCAAGCCATGTCCCTG	1508
QY	1592	TCGCATATGGTTTACAGCTGCTCCGTGATGCTCGAGACAGAGAGGTGTGTGCATTAAGT	1651
Db	1509	TCATTAAGGGTTACAGCTGCTCGATGATTTCCGAGACGAGAGAGGTGTGTGCATTAAGT	1568
QY	1652	CCCCCAGGGTGTACAGTGTGCCCGCTGTGAGCTGTGTGTGATGGCTATTTTGGGGAGCC	1711
Db	1569	CCCCCAGGGGTGTACACGGTGTGCCCTGTGAGCTGTGTGTGATGGCTATTTTGGGGAGCC	1628
QY	1712	CTTGGGGGAACGTGGCCAGTGAAGAGCCCTGACACCCCTGTGATGACCAACAGCAATGTGGA	1771
Db	1629	CTTGTGTGAACATGAGCCCAGTGAAGAGCCCTGTGACACCCCTGTGATGACCAACAGCAATGTGGA	1688
QY	1772	CCCTAGTGCCTCGGGAACTGTGACCGCCTGTGACAGGAGAGTGTCTGAAAGTGCATCCAA	1831
Db	1689	CCCGAGTGCCTCTGGGAATTTGTGACCGCGCTGACAGGAGAGGTGTTGAAGTGTATCCAA	1748
QY	1832	CACAGCTGGGCTCCACTGTGTACCGAGTGAAGCAAGCAGGCTACTATGAGGACCCGTTGGCTCC	1891
Db	1749	CACAGCCGGGCTCTACTGTGCGACGATCCAAAGCAGGCTACTTCCGGGACCCATCGCTCC	1808
QY	1892	CAATTCAGACACAAGGTGAGGTTGCAATTCGAACCCCAAGTGGGCTCGGAGCCCTGTGGA	1951
Db	1809	CAATTCAGACACAAGTGTGAGGCTTGCAACTGTAAACCCATGGGCTCAGAGCCTGTGAGC	1868



OY	1952	GTGTCGAAGTATGGCAGCTGTGTTTGCAGGCCAGGCTTTGGTGGCTCAGCTGTGAGCA	2011
Db	1869	ATGTGGAAGTATGGCACCTGTGTGTTTGCAGGCCAGGATTTGGTGGCCCAACTGTGTGAGCA	1928
OY	2012	TGCGGCACGTGACAGCTGTCCAGCTTCTTAATCAAGTGAAGGTTCCAGATGGATCGATT	2071
Db	1929	TGGAGCACT---CAGCTGTCCAGCTTCTTAATCAAGTGAAGTGAAGTGAAGTGAAGT	1985
OY	2072	TATGCACAGCTCCAGATTCCTGGAGGCCCTGATTTCCAAAGGCTCAGG-----TGAGAC	2125
Db	1986	TATGCACAGCTTCAGAGAAATGAGAGGCCCTGATTTCCAAAGGCTCAGGCTGGTATGGAGT	2045
OY	2126	AGTACCCACGACAGCTGCGAAGGCAGAGATGACAGCGCTGAGCAGGCCCTTCGGGACAT	2185
Db	2046	AGTACCTGATTCACAGCTGCGAAGGCAGAGATGACAGCGCTGAGCAGGCCCTTCAGGACAT	2105
OY	2186	TCCTAGAGAAAGCCAGATTTCACAAAGATGCGTGTAGATCCCTTCAATCCGGGGGGGCCAA	2245
Db	2106	TCCTAGAGAAAGCCAGATTTCACAAAGATGCGTGTAGATCCCTTGTCTCCAGTTGGTCCAA	2165
OY	2246	GGCAAGACACTCCAGAGATAGCTACCCGGGAGCCGCTGGATGACCTCAAGATGATCTGGA	2305
Db	2166	GGTAGAGAGCCCAAGAAACAGCTACAGAGCGGCTGTGATGACCTCAAGATGATCTGGA	2225
OY	2306	AAGAGTTGGGGCCTTGGGACGTCAATACAGAACCAAGTTCAAGATCTCGACGCTCAT	2365
Db	2226	AAGAGTTGGGGCCTTGGGAAAGTCAGTACCAAGAACCGAGTTGGGATCTCAACAGGCTCAT	2285
OY	2366	CACACAGATGGGGCTGAGGCCGTGAGGAAAGTGAAGGCTCCCTGCAAAACCAACATATCC	2425
Db	2286	CACACAGATGGGGCTGAGGCCGTGAGGAAAGTGAAGGCTCCCTGGGAAACATCAATATCC	2345
OY	2426	TCCCTTACAGACACTACACTGGGGCCCAAAATGGCTTTAAAAGTCTGGCTCAGAGAGCCACAG	2485
Db	2346	TGCTTCAGACACACTACAGTGGGGCCCAAAATGGCTTTAAAAGTCTGGCTCAGAGAGCCACAG	2405
OY	2486	ATTGGCAGACAGCCATGTCATGACGCAAGTATACATGAGAGCACTGGCCAAAGAACCA	2545
Db	2406	ATTGGCAGAAAGCCAGCTTGAAGTACAGCCAGTAAACATGAGAGCACTGGCCAAAGAACCA	2465
OY	2546	GGAGTATTTCCAAAGAGTGAATGATACAGTGTGCGGAGGCTCTGTGAGGAAGAG-----G	2599
Db	2466	GGAGTATTTCCAAAGAGTGAATGATACAGTGTGCGGAGGCTCTGTGATGAAGGAGTGGAG	2525
OY	2600	CGGAAGCGGCGACCTTGGACGAGGCCGTGTGTGTCAAAGGCTTTGGGAAAAATGCGAAGAAC	2659
Db	2526	CGGAAGCGGCTGACCCGAGACGCTGTGTGTGTGTCAAAGGCTTTGGGAAAAATGCGAAGAAC	2585
OY	2660	TAAATCTCTGGCCAGAGATTGTGAGGAGGAGCCACGCAACAGCATGGAAGCAGATG	2719
Db	2586	CAAGTCCCTGGCCAGCAGTTGACAAAGGAGGACATCAACGGGAAAAATTGAAGCAGATG	2645
OY	2720	GTCCTTACAGATAGTCTCCACCTTCTCAATTCCTGTGTCTAGATTGAGGAGTCAATGA	2779
Db	2646	GTCCTTACAGACAGTCTCCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2705
OY	2780	TCAGTCCCTGACAGT---AGAAGGAAGAGGCTCAGACAAAAGCTGATTTCTCTCAAA	2836
Db	2706	TCAGTCCCTTTCAGGTGGGAAGAACCAAGAGATCAAAACAAAAGCGATTTACTCTCAAG	2765
OY	2837	CCGTGTGACTAAGCATATGATGATGATTCACAGCAGTGCACAAAGCAATCTGGGAAACTGGGA	2896
Db	2766	CCGTGTATACAGCAGCATATGATGATGATTCACAGCAGTGCACAAAGCAATCTGGGAAACTGGGA	2825
OY	2897	AGAAGAAACCCGCGACGCTTTACAGAAATGGAAGAAATGGGAGACAGACATCAGATCAGCT	2956
Db	2826	AGAAGAAACCAAGACGCTTTACAGAAATGGAAGAAATGGGAGAGAAATCAGATCAGCT	2885
OY	2957	GCTTTCCTCCGCTCCTTGTCTTAAAGCAGAGCCCAAGAACACTAAGTATGGGCAATGC	3016
Db	2886	GCTTTCCTCCGCTCCTTGTCTTAAAGCAGAGCCCAAGAACACTAAGTATGGGCAATGC	2945
OY	3017	CACTTTTTATGAGTGAACATCTTAAAGATCTCAGAGAGTTTGAACCTGCAGGTTGG	3076

[illegible]

XX 09-NOV-2000.  
PD  
XX 28-APR-2000; 2000MO-US11459.  
PF  
XX 30-APR-1999; 99US-0131720.  
PR 21-AUG-1999; 99US-0149738.  
PR 24-SEP-1999; 99US-0155945.  
XX  
XX (BIOS-) BIOSTATUM INC.  
PA  
XX  
PI Boutaud A;  
XX  
XX WPI; 2000-687538/67.  
DR P-PSDB; AAB48468.  
XX  
XX Laminin 5-expressing cells, used to accelerate wound healing associated  
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,  
PT burns, acute wounds and skin grafts -  
XX  
XX Claim 4; Page 175-181; 232pp; English.  
XX  
XX The present sequence encodes a laminin 5 chain polypeptide. Recombinant  
CC laminin 5-expressing cells are used to accelerate wound healing,  
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin  
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations,  
CC gastro-intestinal ulcers, periodontitis, and gingivitis. They are also  
CC used to improve the biocompatibility of medical devices, and to promote  
CC cell adhesion to a surface. They can be used for the ex vivo treatment  
CC of Type I diabetes. Laminin can also be used to regulate angiogenesis.  
CC The cell line produces and secretes recombinant heterotrimeric laminin,  
CC whereas prior art cell lines have been created that produce but do not  
CC secrete only one or two chain laminins.  
XX  
SQ Sequence 5200 BP; 1364 A; 1236 C; 1392 G; 1208 T; 0 other;  
Query Match 74.9%; Score 2986.2; DB 21; Length 5200;  
Best Local Similarity 88.5%; Pred. No. 0;  
Matches 3328; Conservative 0; Mismatches 403; Indels 30; Gaps 7;  
QY 99 AAGGAAAGGAGGACAGCGGAGCGAGAGTGAAGTCCAGCGGCGAGGCGCGGCG 158  
Db 14 AAGGAAAGGAGGACAGCGGAGCGGAGCGGAGTGAAGTCCAGCGGCGAGGCGCGGCG 71  
QY 159 AGCGACCCCTGACGCGCGC-----GACCGCGCGCGCGCGCTGGCCATGCTCGCTCTG 211  
Db 72 AGCGACCCCTGACGCGGAGAGAGAGTGAAGTCCAGCGGCGGCGCGGCGCGCTCGCTCTG 131  
QY 212 GCTGAGCTGCTACCTGCTCTGCTCTGCTCTCTGCGCGGCGGCGGCGGCGGAG 271  
Db 132 GCTGAGCTGCTGCTCTGCTCTGCTCTCTGCGCGGCGGCGGCGGCGGCGGCGGAG 191  
QY 272 GGAAGTCTGATTTGCAAGCGGAGGAGTCCAGAGCAATGATTTGACAGCAATTTACAA 331  
Db 192 GGAAGTCTGATTTGCAATGGAAGTCCAGAGCAATGATTTGATTCGGAATTTACAG 251  
QY 332 ACAGACAGGAATGATTCGCTGCTCTCAACTGCAATGACACACATGATGCACTCAG 391  
Db 252 ACAACTGTGATGATTCGCTGCTCTCAACTGCAATGACACACATGATGCACTCAG 311  
QY 392 CGAGAGTGTGAGGAGGAGATTTACCGAGAGAGAGAGGAGCGCTGTTACCTGCA 451  
Db 312 CGAGAGTGTGAGGAGGAGATTTACCGAGAGAGAGAGGAGCGCTGTTACCTGCA 371  
QY 452 TTGTAAGTCTAAGAGTTCTCTAGCGCTGATGATGCAACTGTGAGGAGGAGGAGTGA 511  
Db 372 TTGTAAGTCTAAGAGGTTCTCTAGCGCTGATGATGCAACTGTGAGGAGGAGGAGTGA 431  
QY 512 GCCAGGTGTGACAGGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 571  
Db 432 ACCAGGTGTGACAGGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 491  
QY 572 TGCTGGGTGCGCCCAAGACCAAGGCTGCTAGACTCCAAAGTGTGACTGTGATGCCAGCTGG 631

Db 492 TCGGGGTGACACCAAGACAGAGAGTGTGATGATGATGATGATGATGATGATGATGAT 551  
QY 632 CATCTCAGGAGCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691  
Db 552 CATCTCAGGAGCCCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 611  
QY 692 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 751  
Db 612 CTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671  
QY 752 CCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 811  
Db 672 CCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 731  
QY 812 TAAATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 871  
Db 732 TAAATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791  
QY 872 GTCTCTGCAAGCTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 931  
Db 792 GTCTCTGCAAGCTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 851  
QY 932 ATCAGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 991  
Db 852 ACTAGATCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911  
QY 992 CGGCGAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1051  
Db 912 TGGGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971  
QY 1052 TGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1111  
Db 972 TGAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1031  
QY 1112 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1171  
Db 1032 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091  
QY 1172 TAAATGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1231  
Db 1092 TAAATGAGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1151  
QY 1232 CCTGCGGATTCGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1291  
Db 1152 CCTGCGGATTCGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1211  
QY 1292 GATTTAGGCGCGCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1351  
Db 1212 GATTTAGGCGCGCGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1271  
QY 1352 TGTGAGCTCAAGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1411  
Db 1272 TGTGAGCTCAAGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1331  
QY 1412 CAGACTGGAAGCTTTGAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1471  
Db 1332 GAGACTGGAAGCTTTGAGCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1391  
QY 1472 TCCAGACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1531  
Db 1392 TCCAGACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1448  
QY 1532 CTGCGCCATTTGTTTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 1591  
Db 1449 CTGCGCCATTTGTTTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAGAGTCAAG 1508  
QY 1592 TCGCAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1651  
Db 1509 TCGCAATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1568  
QY 1652 CCCCCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1711  
Db 1568 CCCCCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1631

Db 1569 CCCTCCGGGGTCACCGGTGCCGCTGTGAGCTCTGTGCTGATGAGCTACTTTTGGGGACC 1628  
QY 1712 CTTGGGGAGAGCTGGCCAGTGGAGGCTTGTGACGCCCTGTCAAGTCAACAACAGCTGGA 1771  
Db 1629 CTTTGGGAACATBGGCCAGTGGAGCTTGTCAGCCCTGTCAATGCAACAGCAATGTGGA 1688  
QY 1772 CCCTAGTGCCTCCGGGAAGCTGACCGCTGACAGGAGGTGTCTGAAATGATCCACAA 1831  
Db 1689 CCCAGTGGCTCTGGGAATGTGTACCGGCTGACAGGAGAGGTGTGAAGTGTATCCACAA 1748  
QY 1832 CACAGCTGGGGTCCACTGTGACAGTGCACAAAGAGGCTACTATGAGGACCCGTTGGCTCC 1891  
Db 1749 CACAGCCGGGCTACTGACGACAGTGCACAAAGGAGGCTACTTGGGGACCATGTGGCTCC 1808  
QY 1892 CAATCCAGACAGAGTGTGAGGCTTCAACTGCACCTGAGGAGCTGGAGGCTGTGGA 1951  
Db 1809 CAACCCAGACAGACAGTGTGAGCTTGCACACTGTAACTGAGGCTGAGGCTGTGAGG 1868  
QY 1952 GTGTGAGAGTGTGAGGCTGTGTGTTGCAAGCCAGGCTTGTGTGGCTCAGCTGTGGA 2011  
Db 1869 ATGTCGAAGTGTGAGGCTGTGTGTTGCAAGCCAGATTTGTGTGGCCCAACTGTGAGCA 1928  
QY 2012 TGGGGCACTGACAGAGCTGTGCTGCTATTAATCAAGTGAAGTTCAAGTGTGATGATG 2071  
Db 1929 TGGAGCAAT--CAGCTGTCCAGCTTGTCTATTAATCAAGTGAAGTGTGATGATGAT 1985  
QY 2072 TATCAGACAGCTCAGATCTGTGAGGAGGCTGTGATTTGCAAGGCTCAGG--TGGAGC 2125  
Db 1986 TATCAGACAGCTTCAAGAGATGTGAGGAGGCTGTGATTTCAAGGCTGAGGCTGTGATGAGT 2045  
QY 2126 AGTACCCAGACAGAGCTGTGAAAGGAGAGATGACAGAGGCTGTGAGAGGCTTGGGAGAT 2185  
Db 2046 AGTACCTGATACAGAGCTGTGAAAGGAGAGATGACAGAGGCTGTGAGAGGCTTGGAGAT 2105  
QY 2186 TCTGAGAGAGGCCAGATTTTCAACAAGTGTCTGTTAGTCTCTCAATCTCCGGGTGGCCAA 2245  
Db 2106 TCTGAGAGATGCCCCAGATTTTCAAGAGTGTCTGACAGATCTCTGTGCTTCCAGTTGGCCAA 2165  
QY 2246 GGCAGAGACTCAAGAGATAGCTACCGGAGCCGCTGATGACCTCAAGATGACTGTGGA 2305  
Db 2166 GGTGAGAGGCCAAGAGAGAGCTACAGAGGCGCTGATGATCTCAAGATGATGTGTGA 2225  
QY 2306 AAGAGTTCCGGGCTGTGGGAGTCAATACAGAACCAAGTTGAGAGTACTGCGAGGCTCAT 2365  
Db 2226 AAGAGTTCCGGGCTGTGGGAGTCAATACAGAACCGAGTTCCGAGTACTGACAGGCTCAT 2285  
QY 2366 CACACAGATGGGCTGTGAGGCTGTGAGAGAAAGTGAAGCTTCCCTGCAAAAACACACATTTCC 2425  
Db 2286 CACACAGATGAGCTGTGAGGCTGTGAGAGAAAGTGAAGCTTCCCTGCAAAAACACATTTCC 2345  
QY 2426 TCCCTCAGAGACTAGCTGTGGGCAAAATGCTTTAAAGTGTGGCTCAGAGGCGACAGAG 2485  
Db 2346 TCCCTCAGAGACTAGCTGTGGGCAAAATGCTTTAAAGTGTGGCTCAGAGGCGCACAGAG 2405  
QY 2486 ATTGGCAGACAGCATTTTCACTAGTACGCCAGTAACTGAGAGCACTGCGCAAGAAACCCA 2545  
Db 2406 ATTGGCAGAAAGCCAGCTGTGAGTACGCCAGTAACTGAGAGCACTGACAAAGGAAACTGA 2465  
QY 2546 GGATATTTCCAAAGAGCTGATGTCACTGTGCGGAGGCTGTGAGAGAAAGAG--G 2599  
Db 2466 GGATATTTCCAAAGAGCTGATGTGTGCGGAGGAGGCTGTGATGTAAGAGTGTGCGAAG 2535  
QY 2600 CGGAAGGCGGAGCTGTGAGGAGGCGGTGTGCAAGAGGCTTGTGGGAAATTTGCGAAGAAC 2659  
Db 2526 CGGAAGGCGGTAGCCCGGAGGCTGTGTGTGTCAAGAGGCTTGTGAAATTTGGAGAAAGAC 2585  
QY 2660 TAAATCTGTGCGCCAGAGATTTGTGAGAGGAGCCACGCAAAACGACATGGAAGCAGATG 2719  
Db 2586 CAATGCTGCGCCAGCAGATTTGCAAGAGGAGGCCACATCAACGGAATTTGAAGCAGATGAG 2645  
QY 2720 GTCTTATCAGATAGTGTCCACCTTCTCAATTCCTGTGTCTCAGATTCAGGAGATCAATGA 2779  
Db 2646 GTCTTATCAGCAGATGTCCGCTCTCGATTCAGTGTCTCCGCTTCAGGAGATCAGTGA 2705

QY 2780 TCACTCCTTGCAAGT---AGAAGGAGAGGCTCAGACAAAGAAAGCTGATCTCTCAAA 2836  
Db 2706 TCACTCCTTTCAGGTGGAAGAGCAAGAGATCAACAAAGGATTCACCTCTCAAG 2765  
QY 2837 CCGTGTGACTAGCATATGATGATGATTTCAAGCAGCTGCAAGACATCTGGGAAATCTGGGA 2896  
Db 2766 CCTGTTAACCAAGCATATGATGATGATTTCAAGCGTACAAAGAAAGATCTGGGAAATCTGGAA 2825  
QY 2897 AGAAGAAACCCGGGAGCTCTTACGAATGGAAGAAATGGAAGACAGATCAATCAATCACTG 2956  
Db 2826 AGAAGAAAGCAGAGAGCTCTTACAGATGGAAGAAAGTGGAGAGAGAAATCAATCAATCACTG 2885  
QY 2957 GCTTCCCGTCCCAACCTTGTCTTAAAGCAGAGCCCAAGAGCACTAATGATGAGCAATG 3016  
Db 2886 GCTTCCCGTCCCAATTTGTCTTAAAGCAGAGCAAGAGCACTAATGATGAGCAATG 2945  
QY 3017 CACTTTTATGAAAGTGAAGACATCTTAAAGAAATCTCAGAGATTTGACCTGCAAGTTGG 3076  
Db 2946 CACTTTTATGAAAGTGAAGACATCTTAAAGAACTCAGAGATTTGACCTGCAAGTTGG 3005  
QY 3077 AGATTAAGAGCAAGACCTGAAGAGGCAATGAAGAGATCTCCATCAATGAGCCAGAGAT 3136  
Db 3006 CAACGAAAGAGCAGAGCTGAAGAGGCAATGAAGAGATCTCTTACATCAAGCAGAGAGT 3065  
QY 3137 TGCAGTGTCCAGTGTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3196  
Db 3066 TTTGAGATGCGCAGTACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3125  
QY 3197 CGCCAGAGAGGCAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3256  
Db 3126 TGCACAGAGAGGCAAGAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3185  
QY 3257 GGAGATGAGAGAGAGTGAAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3316  
Db 3186 GGAGATGAGAGAGTGAAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3245  
QY 3317 GAAAGAGAGTGGCCACTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3376  
Db 3246 AAGAGAGAGTGGCCCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3305  
QY 3377 GGAGCAGAGATTTTACATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3436  
Db 3306 GGAGCAGAGATTTTACATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3365  
QY 3437 AGTGAAGAAACAGAGCAGT 3496  
Db 3366 GGTGATGATCAGT 3425  
QY 3497 TGGCATCTTACACCTAATAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3556  
Db 3426 CGGCTCCTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3485  
QY 3557 GGAGCAGAGAGATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3616  
Db 3486 GGAGCAGAGAGATTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3545  
QY 3617 AGAGCTGGAAGT 3676  
Db 3546 AGAGCTGGAAGT 3605  
QY 3677 AGATGAGAGATTTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3736  
Db 3606 AGATGAGAGATTTTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3665  
QY 3737 CTGCTACAAATCCAGT 3796  
Db 3666 CTGCTACAAATCCAGT 3725  
QY 3797 GGTCTTGGAGATGAGT 3837  
Db 3726 GGTCTTGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 3766

ID	Accession	Standard	CDNA	BP
XX	AA142910	standard	CDNA	5200 BP
XX	AA142910			
XX	AA142910			
XX	05-AUG-2002	(first entry)		
XX				
DE	Laminin gamma-2 chain CDNA sequence 1.			
XX				
KW	laminin gamma-2; gene; ss; cancer; laminin gamma-2 chain inhibition;			
KW	carcinogen inhibition; anti-gamma-2 chain antibody;			
KW	epithelial cell adhesion; laminin-5.			
XX				
OS	Unidentified.			
XX				
FH	Key	Location/Qualifiers		
FH	CDS	118..3699		
FT		/tag= a		
FT		/product= "Laminin gamma-2 chain 1"		
FT	sig_peptide	118..183		
FT		/tag= b		
FT	mat_peptide	184..3696		
FT		/tag= c		
FT		/note= "Mature laminin gamma-2 chain 1"		
XX				
PN	US2002052307-A1.			
XX				
PD	02-MAY-2002.			
XX				
PF	08-JAN-2001; 2001US-0756071.			
XX				
PR	07-JAN-2000; 2000US-175005P.			
PR	04-OCT-1994; 94US-0317450.			
PR	18-FEB-1997; 97US-0800593.			
PR	15-SEP-2000; 2000US-0663147.			
XX				
PA	(TRYG/) TRYGVASON K.			
PA	(KALL/) KALLUNKI P.			
PA	(PYKE/) PYKE C.			
XX				
PI	Trygvason K, Kallunki P, Pyke C;			
XX				
DR	WPI; 2002-434824/46.			
DR	P-PSDB; AAO14692.			
XX				
PT	Modulating laminin 5 gamma 2 chain interactions of invasive carcinogens			
PT	for treating cancers and promoting attachment of cultured cells in			
PT	vitro -			
XX				
PS	Example 1; Fig 4; 51pp; English.			
XX				
CC	The invention comprises a method of inhibiting the laminin gamma-2 chain			
CC	interactions of invasive carcinogens with surrounding tissues - by using			
CC	anti-gamma-2 chain antibodies to inhibit the gamma-2 chain biological			
CC	activity of the invasive carcinogens. The invention also comprises a			
CC	method for promoting adhesion of epithelial cells by exposing the cells			
CC	to interact laminin-5 molecules. The first method of the invention is			
CC	useful for preventing gamma 2 chain interactions of invasive carcinogens			
CC	with surrounding tissues. The second method of the invention is useful			
CC	for promoting adhesion of cultured epithelial cells. The present CDNA			
CC	sequence encodes a laminin gamma-2 chain.			
XX				
SQ	Sequence 5200 BP; 1364 A; 1236 C; 1392 G; 1208 T; 0 other;			
XX				
0Y	Query Match	74.9%; Score 2986.2; DB 24; Length 5200;		
0Y	Best Local Similarity	88.5%; Pred. NO. 0;		
0Y	Matches 3128; Conservative	0; Mismatches 403; Indels 30; Gaps 7		
0Y	99 AAGGAAAGGAAGGACACGACGCGGAGCGGAGAGAGAACTCCAGCGGCGGAGCGCGGC 158			
0Y				
0Y	14 AAGGAAAGGAAGGACACGCGGAGCGGAGAGAGAAACCAAC--CGAGCGCGCGGC 71			

OY	159	AGCGACCCCTTCAGCGGGG-----GACCGCGGGCGGGCCCTGGGCAATGCTGGGCTG	211
Db	72	AGCGACCCCTTCAGCGGGGAGACAGACTGACGGCGCGGACCGCATGCTGGGCTG	131
OY	212	GCTGAGCTGCTACCCCTGCTTCTTGAGCTCTCTGCGCGGACCGCGGGCACCTCGGGAG	271
Db	132	GCTGGGCGTGGCCCTGCTCTTCTTGCTCTCTGCGGACCGCGGGCACCTCGAGAG	191
OY	272	GGAAGTCTGTGATTGCAACGGGAAGTCCAGCAATGCATCTTTGACCAAGCACTTCACAA	331
Db	192	GGAGTCTGTGATTGCAATGGGAAGTCCAGCGAGTGTATCTTTGATCGGGAATCTCACAG	251
OY	332	ACAGACGAAGTAATGGATTCGCGTGCCTCACTGCAATGACAACATGTGATGATCACTG	391
Db	252	ACAAACTGTGTAATGGATTCCGCTGCTCACTGCAATGACAACATGTGATGATCACTG	311
OY	392	CGAGAGGTGCAAGGACAGGATTTTACCGACAGAGAAAGGAGCGGCTGTTACCGCTGC	451
Db	312	CGAGAGGTGCAAGATGGCTTTTACCGGACAGAGAAAGGAGCGGCTGTTACCGCTGC	371
OY	452	TTGTAACTCTAAAGTTCCTTTAGCGCTCCATGTGACAACTCTGGAGGGTCCACTGTAA	511
Db	372	TTGTAACTCCAAAGTTCCTTTAGTGTGCAATGTGACAACCTCTGGAGGGTCCACTGTAA	431
OY	512	GCCAGGTGTGACAGAGACAGTGTGACGATGTCTGCGCGGCTTCCACACACTTCAC	571
Db	432	ACCAAGTGTGACAGAGACCAATGACCAATGTCTGCGAGGCTTCCACATGCTCACGGA	491
OY	572	TGCTGGGTGCCCCAAGACCAAGGCTGTAGACTCCAAGTGTGATGATGCCAGCTGG	631
Db	492	TGCGGGGTGACCCCAAGACCAAGACTGTAGACTCCAAAGTGTGATGATGCCAGCTGG	551
OY	632	CATCTCAGAGGCCCTGTGACTAGGCCCGCTGTGTCTGCAAGCCGGGCTGTCACTGGAGAGC	691
Db	552	CATGCGAGGGGCCCTGTGAGCGGGGCGGCTGTGTCTGCAAGCCAGCTGTACTGGAGAGC	611
OY	692	CTGTGAATAGGTGACAGAGGTATCTATACACTGGATGGGGAAACCTCAGGGGCTGTAC	751
Db	612	CTGTGAATAGGTGTGATCAGAGGTATCTATATCTGGATGGGGAAACCTCAGGGGCTGTAC	671
OY	752	CCAGTGTGTTTGTATGGGCAATCCGCCAGCTGCCACAGCTCTGGGGCACTACAGTGTCCA	811
Db	672	CCAGTGTGTTTGTATGGGCAATCCAGGCAATGTTGAGGCGGAAGGCTGTCCAAAGAACG	731
OY	812	TAAATATATCTCTGCTCCATCAAGATGTTGATGGGCGGAAGGCTGTCCAAAGAACG	871
Db	732	TAAATATATCTCTACCTTTCACTCAAGATGTTGATGGGCGGAAGGCTGTCCAAAGAACG	791
OY	872	GTCCTCTGCAAGCTCCAGTGTGACACAGCGGCATCGGGATATATTATAGCTTCAGCAGCAG	931
Db	792	GTCCTCTGCAAGCTCCAAATGTCACAGCGGCATCAAGATGTGTTAGCTTCAGCAGCAGC	851
OY	932	ATCAGACCCCTGTATTTTGTAGCTCCTGCCAAATTTCTTGGGAATCAACAGGTGAGCTA	991
Db	852	ACTGATGCTGTCTATTTTGTGGCTCCTGCGCAAAATTTCTTGGGAATCAACAGGTGAGCTA	911
OY	992	CGGGCAAGGCTATCTTTTGTACTACGCGTGTGATAGGGGAGGCAAGCACCCATCTGCCCA	1051
Db	912	TGGGCAAGGCTGTCTTTTGTACTACCGTGTGATAGGAGGAGGCAAGCACCCATCTGCCCA	971
OY	1052	TGAGCTGATCTGGAAGGTGCTGTGTCACGGATCACAGCTCCCTTGATGCCACTTACCA	1111
Db	972	TGATGTGATCTCTGGAAGGTGCTGTGTCACGGATCACAGCTCCCTTGATGCCACTTACCA	1031
OY	1112	GACACTGCTTGTGGGATCACCAAGACTTACACATTCAGATTAAATGAACTCCACAGCAG	1171
Db	1032	GACACTGCTTGTGGGCTCACCAAGACTTACACATTCAGGTTAAATGAGCATTCACAGCAA	1091
OY	1172	TAAATTGGAGCCCCAGGCTAAGTATCTTGAATATCGGAGGTTACTGGGAACTCTCACAGC	1231
Db	1092	TAAATTGGAGCCCCAGGCTAAGTATCTTGAATATCGAAGGTTACTGGGAAATCTCACAGC	1151

QY	1232	CTCGGGATCCGAGCTACCTACGGAGAAATACAGTACTGGGTACATTGACAACGTCGACTT	1291
Db	1152	CCTCCGATCCGAGACTACATATGAGAAATACAGTACTGGGTACATTGACAATGTGACCTT	1211
QY	1292	GATTTCAGCCCGCCCGCTTCTGTGAGGCCACGCCCCCTGGGTTGAACAATGTGTATGCC	1351
Db	1212	GATTTCAGCCCGCCCGCTTCTGTGAGGCCACGCCCCCTGGGTTGAACAATGTGTATGCC	1271
QY	1352	TGTTGGGTACAAAGGGGAGTGTCTCCACGAGTATGTCTCCGGTACCAAAAGATGTAGC	1411
Db	1272	TGTTGGGTACAAAGGGGAGTATGTCTCCACGAGTATGTCTCTTGACTACAAAGAGATTTAGC	1331
QY	1412	CAGACTGGGACCTTTTGGACCTGTATTCATGTAACTGCCAAGGGGAGGGGCGCTCGA	1471
Db	1332	GAGACTGGGGCGCTTTTGGACCTGTATTCCTTGTAACTGTCAAGGGGAGGGGCGCTGTGA	1391
QY	1472	TTCAGACACAGSAGACTGTACTACGAGGGAGTANAACCTTGACATCCCTCAGTGTGTGA	1531
Db	1392	TTCAGACACAGSAGATTTGTATTTACGGGGATGANAATCTCTGACAT---TGAGTGTGTGA	1448
QY	1532	CTGGCCCATTTGGTTTCTACAAAGATTCACAAGACCCCCCGCAGCTGCAAGCGCTGCCCTG	1591
Db	1449	CTGGCCCATTTGGTTTCTACAAAGATTCGCGACAGACCCCCGACGCTGCAAGCATTCCTGTG	1508
QY	1592	TCCGAATATGGTTACAGCTGTCTCCGTGATTCCTGAGACAGAGAGGAGTGTGTCAATAACTG	1651
Db	1509	TCATTAACGGGTTTCAGCTGTCTCAGTGATTTCCGAGACGGAGAGAGTGTGTCAATAACTG	1568
QY	1652	CCCCCAGGTTTCACTGGTGGCCCGCTGTGAGCTGTGTCTGTATGTGGCTATTTTGGGACCC	1711
Db	1569	CCCCCGGGGTTCACTGGGTGGCCCGCTGTGAGCTGTGTCTGTATGTGGCTATTTTGGGACCC	1628
QY	1712	CTTGGGGGAAGTGGCCAGTGAAGGAGCGCTTGTACACCCCTGTACGTGCAACAACAGCTGGA	1771
Db	1639	CTTGTGTGAACATATGGCCAGTGAAGGAGCGCTTGTACACCCCTGTATGTCAACAGCAATGTGGA	1688
QY	1772	CCCTAGTGCCTCCGGGAACTGTGTGACCGCCTGACAGGAGGTGTCTGAAGTGCATCCACA	1831
Db	1689	CCCCAGTGCCTCTGTGGAAATTTGTGAACCGGCTGACAGGAGGTGTGAAGTGTATCCACA	1748
QY	1832	CACAGCTBTGGGTTCCACTGTGTACCAAGTGCANAAGCAGGCTACTATGGGGACCCGTTGGCTCC	1891
Db	1749	CACAGCCGGGCACTACTGTGCGACAGCTGCANAAGCAGGCTACTTCCGGGGACCCATTGGCTCC	1808
QY	1892	CAATCCAGACAGCAAGGTGTGAGGTTGTGAACCCAGTCAGTGGGCTGCGAGCGCTGTGGA	1951
Db	1809	CAATCCAGACAGCAAGTGTGAGGTTGTGAACCCAGTCAGTGGGCTGCGAGCGCTGTGAGG	1868
QY	1952	GTGTGCAAGTATGGCAGCTGTGTTTTTCGAACCCAGGCTTGTGGGCTCAGCTGTGAGCA	2011
Db	1869	ATGTGCAAGTATGGCAGCTGTGTTTTTCGAACCCAGGATTTGTGTGGCCCAACTGTGAGCA	1928
QY	2012	TGCGGCACTGACCAAGCTGTCTCAGCTTGTCTATATCAAGTGAAGTTCCAGATGATCAGTT	2071
Db	1929	TGAGGCACTT---CAGCTGTCTCAGCTTGTCTATATCAAGTGAAGTATTCAGATGATCAGTT	1985
QY	2072	TATGACAGAGCTCCAGATCCTGGAGGCCCTGATTTTGAAGGCTGAGGG-----TGAGC	2125
Db	1986	TATGACAGAGCTTTCAGAGATGTGAGGCCCTGATTTTCAGAGGCTGAGGGTGTGTATGAGT	2045
QY	2126	AGTACCCACAGCAGAGCTGTGAAGGCGAGATCAGCAGGCTGTGAGCAGGCGCTTCCGAGCAT	2185
Db	2046	AGTACCTGATATCAAGAGTGTGAAGGCGAGATTCACAGAGGCTGTGAGCAGGCGCTTTCAGCAT	2105
Db	2106	TCTAGAGAGTCCAGATTTTCAGAAAGTGTGATGATCCCTTGTGTCTCCAGTGTGCCAA	2165
QY	2246	GGCAAGAGCTCAAGAGATTAAGTCCGGGAGCGGCTGGATATGACTCAAGATGATGTGGA	2305
Db	2166	GGTGTAGGCAAGAGATTAAGTCCAGAGCGGCTGGATATGACTCAAGATGATGTGGA	2225
QY	2306	AAGAGTTCCGGCCCTTGGCACTGTATTCACAAACCAAGTTGAGATGACTCCAGAGCTCAT	2365

Db	2226	AAGATTCTGGGCTCTGGGAAGTCACTACCAAAACCGAGTTGGGATACTCACAGGCTCAT	2285
QY	2366	CACATCAGATGGGCTGAGACCTGGAGAAAGTGAAGGCTTCCTCGCAAAAACCAACATTTCC	2425
Db	2286	CACATCAGATGGAGCTGAGACCTGGGAGAAAGTGAAGCTTCTTTGGGAAAACTCAATATTTCC	2345
QY	2426	TCTCTTCAGAGCACTACAGCGGGGGCCAAATGCGTTTAAAGTTGTGGCTCGAGAGGCGACAG	2485
Db	2346	TGCTTCAGAACCACTACGTTGGGGGCCAAATGCGTTTAAAGTTGTGGCTCGAGAGGCGACAG	2405
QY	2486	ATTGGCAGACACCATGTTCACTCAGTCAGCCAGTAAACATGGAGCACTGGCCAAAGAACCCA	2545
Db	2406	ATTGAGCAAAAGACCAAGCTTTGAGTCAAGCCAGTAAACATGGAGCACTGGCAAGGAAACTGA	2465
QY	2546	GGAGATTTCCAAAAGCTGATGATCTACGTGTGCGGGAGGCTGTGGAGAAAGG-----G	2599
Db	2466	GGACTATTCCAAACAGACCCCTCTCACTGTGTGCGCAAGGCCCTGTGATGAAGGAGTCCGAG	2525
QY	2600	CGGAAGCGGACCGCTGAGCGGAGGCGTGTGTCAAAGAGCTTGTGGGAAATTTGCAGAAAC	2659
Db	2526	CGGAAGCGGATGCCCCGAGCGGTGCTGTGTGTCAGAGGCTTGTGAAAAATTTGGAGAAAC	2585
QY	2660	TAAATCTCTGGCCCCAGAGTTGTGAGGGAGGCCAAGCAACCGACATGAGAGAGATAG	2719
Db	2586	CAAGTCCCTGGCCCCAGAGTTGAGACAAAGGAGGACCACTCAACGCGAAATTTGAAGCAGATAG	2645
QY	2720	GCTTTATACAGATAGTCTCCACACTTTCATTTCCGTGTCTCAAGATTCAGGAGTCATAGA	2779
Db	2646	GCTTTATACAGACACTCTCCGCTCTCTGTGATGATGTCTCTCCGTCTGGGAGTCACTAGA	2705
QY	2780	TCAGTCTCTTGAGAGT---AGAAGCGAAGAGGCTCAGACAAAAAGCTGATTTCTCTCAAA	2836
Db	2706	TCAGTCTCTTGAGAGTGAAGAAAGCAAGAGGATCAACAAAAAGCGATTCACTCTCAG	2765
QY	2837	CCGTGTGACTAAGCATATGATGATGATTCAGACAGTGCAGAAACATCTGGGAAACTGGGA	2896
Db	2766	CCGTGTGACTAAGCATATGATGATGATTCAGACAGTGCAGAAAGATCTGGGAAACTGGGA	2825
QY	2897	AGAAGAAACCCGGGAGCTCTTACAGATGGAAGAAAGTGGGAGACAGACATCAGATCAGCT	2956
Db	2826	AGAAGAAACCAAGCAGCTTACAAATGGAAGAAAGTGGGAGAGGAATCAGATCAGCT	2885
QY	2957	GCTTTCCTGGGCAACCTTGTCTAAAGAGAGGCCCAAGACAGTCAATATGAGGCAATGC	3018
Db	2886	GCTTTCCTGGGCAACCTTGTCTTAAAGAGAGGCCCAAGACAGTCAATATGAGGCAATGC	2945
QY	3017	CACATTTTATGAAGTTGGAACATCTTAAAGATCTCGAGAGTTTGAACCTGCAGGTTGG	3076
Db	2946	CACATTTTATGAAGTTGAGAGCATCTTAAAGACCTCAGAGGTTTGAACCTGCAGGTTGG	3005
QY	3077	AGATTAAGAGCAGAGCTGAAAGAGCCATGAAGACTCTCTCATCAGCCAGAAAGT	3136
Db	3006	CACAGAAACAGAGAGCTGAAAGAGCCATGAAGAGCTCTCTCATCAGCCAGAAAGT	3065
QY	3137	TGCAGGTGCTCAGTGCAGAGAGCAAGCAGACAGCACCCCTGGGCACTGTGCTGCCGGA	3198
Db	3066	TTCAGATCCAGTGCAGAGAGCCAGACAGCAAGAAAGAGCCCTGGGAGAGCGTGTGCTGCA	3125
QY	3197	CGCCAGAGGGCAAAAGATGCAAGCCAGGAGGAGCCCTGGAGATCTCTGGCAAGATAGACA	3256
Db	3126	TGCACAGAGGGCAAAAGATGAGGGGAGGAGGAGCCCTGGAAATCTCAATGAGATTAAGACA	3185
QY	3257	GGAGATTGAGAGTCTGAACTTGAAGCCATATGTGACAGCAATGAGAGCTTGGCCATGGA	3316
Db	3186	GGAGATTGAGAGTCTGAACTTGAAGCCAAATGTGACAGCAATGAGAGCTTGGCCATGGA	3245
QY	3317	GAAAGGAGTGGCACTGTGAAGAAAGGAGATGAGAAATGGAAGAGAGCTGTCAAGAA	3378
Db	3246	AAAGGAGTGGCTCTCTGAAAGAGTGAATGAGGAAAGTGCAGAGAGAGCTTGGAAAGGA	3305
QY	3377	GGAGAGGAGTGTGACATGATGATGAGCAGCAGTGCAGATGGTAAATTGCAAGGCCCAAG	3436

Db 3306 GGAGCTGGAGTTGACACGATATGATGCTAGACAGATGTTGATTTACAGAACCCAGAA 3365  
QY 3437 AGTTGAAAACAGAGCCAGAAATGCTGAGTTTACGATCCAGACACACTCAACACATTGGA 3496  
Db 3366 GGTGATACCAAGAGCCAGAAACGCTGGGTTTACATCAAGACACACTCAACACATTGGA 3425  
QY 3497 TGGCATCTTACACTTAATAGACAGCTGGCACTGTGGATGAAGAGAGGCTGATCTTACT 3556  
Db 3426 CGGCTCTCTGATCTGATGACAGCCCTCAGTGTAGATGAAGAGAGGCTGATCTTACT 3485  
QY 3557 GGAGCAGAAAGCTTTTCCGAGCCAAAGACTCAGATCAACAGCCAGCTGAGCCCTTATGTC 3616  
Db 3486 GGAGCAGAAAGCTTTTCCGAGCCAAAGACTCAGATCAACAGCCAGCTGAGCCCTTATGTC 3545  
QY 3617 AGAGCTGGAAGAGAGGACACATCGGCAAGAGGCGCACCTCGTTCTCTGAGACTAGCAT 3676  
Db 3546 AGAGCTGGAAGAGAGGACACATCGGCAAGAGGCGCACCTCGTTCTCTGAGACTAGCAT 3605  
QY 3677 AGATGGGATTCCTGCTGATGTGAAGAACCTGGAAGAACATGAGGACAACTGCCCCGGG 3736  
Db 3606 AGATGGGATTCCTGCTGATGTGAAGAACCTGGAAGAACATGAGGACAACTGCCCCGGG 3665  
QY 3737 CTGCTCAATATACCCAGGCTCTTGAAGCAACAGTGAAGCTGCTTGAAGATTTCTCAACCA 3796  
Db 3666 CTGCTCAATATACCCAGGCTCTTGAAGCAACAGTGAAGCTGCTTGAAGATTTCTCAACCA 3725  
QY 3797 GGTTCCTGGGATTGACAGCTAGCTGCTTGAAGATTTCTCA 3837  
Db 3726 GGTTCCTGGGATTGACAGCTAGCTGCTTGAAGATTTCTCA 3766

RESULT 4  
AAC65866  
ID AAC65866 standard; cDNA; 5156 BP.

XX AAC65866;  
XX  
XX 21-FEB-2001 (first entry)  
XX  
XX Human lung cancer-associated cDNA for contig 20.  
XX  
XX Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;  
XX  
XX vaccine; detection; ss.  
XX  
XX Homo sapiens.  
XX  
XX MO200061612-A2.  
XX  
XX 19-OCT-2000.  
XX  
XX 03-APR-2000; 2000WO-US08896.  
XX  
XX 02-APR-1999; 99US-0285479.  
XX  
XX 17-DEC-1999; 99US-0466396.  
XX  
XX 30-DEC-1999; 99US-0476496.  
XX  
XX 10-JAN-2000; 2000US-0480884.  
XX  
XX 22-FEB-2000; 2000US-0510376.  
XX  
XX (CORI-) CORIXA CORP.  
XX  
XX Wang T, Fan L;  
XX  
XX WPI; 2000-628399/60.  
XX  
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor  
XX  
XX protein is used for detecting and monitoring progression of lung cancer  
XX  
XX in a patient -  
XX  
XX Claim 25a; Page 152-153; 261pp; English.  
XX  
XX This invention describes a novel isolated polypeptide (I) which  
XX  
XX comprising an immunogenic portion of a lung tumor protein or variant (P2)  
XX  
XX which have cytostatic activity. The polypeptides and polynucleotides are

CC used in compositions and vaccines to inhibit the development of cancer,  
CC especially lung cancer, in a patient. Methods described in the invention  
CC can be used to monitor the progression of a cancer by carrying out the  
CC detection at subsequent time points and comparing the results from the  
CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient  
CC are treated with P2, polynucleotides encoding P2 or antigen presenting  
CC cells expressing P2 and then administered to the patient to inhibit  
CC development of cancer.  
XX  
SQ Sequence 5156 BP; 1351 A; 1222 C; 1377 G; 1206 T; 0 other;  
Query Match 74.1%; Score 2956.4; DB 21; Length 5156;  
Best Local Similarity 88.4%; Pred. No. 0;  
Matches 3285; Conservative 0; Mismatches 401; Indels 28; Gaps 6;  
QY 146 CGAGGGCGGGGCGAGGACCCCTGACGCGCG-----GACCGCGCGCGCGTGGCCA 198  
Db 7 CGAGGGCGGGGCGAGGACCCCTGACGCGGAGACAGACTAGCGCGCGCGCGCGCA 66  
QY 199 TGGCTGCGCTGCTGAGCTGCTACCTGCTTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 258  
Db 67 TGGCTGCGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 126  
QY 259 CCACCTCCGGGAGGGAAGTCTGTGATGGAAGGGAAGTCCAGGCAATGATCTTGGAC 318  
Db 127 CCACCTCCAGGAGGAAGTCTGTGATGGAAGGGAAGTCCAGGCAATGATCTTGGATC 186  
QY 319 AGGAAGCTTCAACAGAGAGAGGAATGATTCGCTGCTCACTCAATGACACACTG 378  
Db 187 GGGAACTTCAACAGAGAGAGGAATGATTCGCTGCTCACTCAATGACACACTG 246  
QY 379 ATGGCATCCACTGCGAGAGGCTGCAAGAGATTTTACGACAGAGAGAGAGAGAGAGAGAG 438  
Db 247 ATGGCATTCAGCTGCGAGAGGCTGCAAGAGATTTTACGAGAGAGAGAGAGAGAGAGAG 306  
QY 439 GTTTACCTGCAATTTGAACTGTAAGGTTCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 498  
Db 307 GTTTGCTGCTGCAATTTGAACTGTAAGGTTCTTTCGCTGCTGCTGCTGCTGCTGCTGCTGCT 366  
QY 499 GGTGAGCTGTAAAGGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558  
Db 367 GGTGAGCTGTAAAGGCTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426  
QY 559 ACACACTCACTGATGCTGGGTGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 618  
Db 427 ACATGCTCAAGATGGGGGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486  
QY 619 GTGACCCAGCTGATCTGAGGCGCTGTGACTCAGAGCGCTGTGCTGCTGCTGCTGCTGCTGCT 678  
Db 487 GTGACCCAGCTGATCTGAGGCGCTGTGACTCAGAGCGCTGTGCTGCTGCTGCTGCTGCTGCT 546  
QY 679 TCACTGAGAGCGCTGTGATAGGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 738  
Db 547 TCACTGAGAGCGCTGTGATAGGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606  
QY 739 CTGAGGCTGTACCCAGCTGTTCTGCTATGAGGAGATTGACAGCACTCCGAGCTGTGACG 798  
Db 607 CTGAGGCTGTACCCAGCTGTTCTGCTATGAGGAGATTGACAGCACTCCGAGCTGTGACG 666  
QY 799 ACTAGAGTGCATTAATATCATCTGCTTCCATCAAGATGTTGATGAGTGGAGAGCTG 858  
Db 667 AATACAGTGCATTAATATCATCTGCTTCCATCAAGATGTTGATGAGTGGAGAGCTG 726  
QY 859 TCCAAAGAAACGGGCTCTGCAAGAGCTCAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAG 918  
Db 727 TCCAAAGAAATGGGCTCTGCAAGAGCTCAGTGTGACAGAGAGAGAGAGAGAGAGAGAGAG 786  
QY 919 GCTCAGCAGAGATGAGACCTGTCTATTTTGTACTCTGCAAAATTTCTTGGAGATC 978  
Db 787 GCTCAGCAGCAGATGAGACCTGTCTATTTTGTACTCTGCAAAATTTCTTGGAGATC 846  
QY 979 AATAGTGTAGCTAGGAGCAAGAGCTTCTTTTACATACGCTGTGATAGGAGAGAGAGAG 1038

Db 847 AACAGGTGAGCTATGCTCAAAAGCTGTCTTGTACTACCTGTGACACAGAGGACGAC 906  
Qy 1039 ACCCATCTGCCATGAGCTGATCTGGAAGGTGCTGTCTACGAGTACACAGCTCCCTTGA 1098  
Db 907 ACCCATCTGCCATGAGTGTATTTCTGGAAGGTGCTGTCTACGAGTACACAGCTCCCTTGA 966  
Qy 1099 TGGCAGTTGACAGACACAGCTGCTTGTGGAGTACACCAAGACTTACACATTCAGATTAAATG 1158  
Db 967 TGGCAGTTGACAGACACAGCTGCTTGTGGAGTACACCAAGACTTACACATTCAGATTAAATG 1026  
Qy 1159 AACATCCAGAGATTAATTTGAGAGCCCAAGCTAAATTTACTTTGATATCGAGGTTACTGC 1218  
Db 1027 AGCATTCAGAGCAATTAATTTGAGAGCCCAAGCTAAATTTACTTTGATATCGAGGTTACTGC 1086  
Qy 1219 GGAATCTCAGAGCCCTCGGAGTCCGAGTACCTACGAGGATTAAGTACAGTGGTATACATG 1278  
Db 1087 GGAATCTCAGAGCCCTCGGAGTCCGAGTACCTACGAGGATTAAGTACAGTGGTATACATG 1146  
Qy 1279 ACAAGCTGACCTTGAATTTACAGCCCGCCGTTTCTGAGAGCCCAAGCCCTGAGGTTGAC 1338  
Db 1147 ACAATGTGACCTTGAATTTACAGCCCGCCGTTTCTGAGAGCCCAAGCCCTGAGGTTGAC 1206  
Qy 1339 AATGTGATGCTGCTGTTGAGTACAAAGGAGGAGTCTGCAAGATTTGCTTCCGCTTACA 1398  
Db 1207 AGTGTATATGCTGCTGTTGAGTACAAAGGAGGAGTCTGCAAGATTTGCTTCCGCTTACA 1266  
Qy 1399 AAGAGATTCAGCCAGACCTGGAGCTTTTGGACCTGTATTCATCTGATTAACCTGCAAGGG 1458  
Db 1267 AGAGATTCAGCCAGACCTGGAGCTTTTGGACCTGTATTCATCTGATTAACCTGCAAGGG 1326  
Qy 1459 GAGGGGCTGCGCTGACAGACAGAGAGAGTCTTACTACGAGGAGTACAGAACCTGACATCC 1518  
Db 1327 GAGGGGCTGCGCTGACAGACAGAGAGAGTCTTACTACGAGGAGTACAGAACCTGACATCC - 1384  
Qy 1519 CTGAGTGTGCTGACTGCCCCCTTTGTTTCTTACAAAGATCCCAAGAGCCCCCGAGCTGCA 1578  
Db 1385 -TGAGTGTGCTGACTGCCCCCTTTGTTTCTTACAAAGATCCCAAGAGCCCCCGAGCTGCA 1443  
Qy 1579 AGCGGTGCCCCCTGTGCAATGAGGTTTCAAGCTGCTCCGATGCTGAGAGCAGAGAGGAGTGG 1638  
Db 1444 AGCGATGTCCCTGTCTATACAGGAGTCTTCACTGCTCAATGATGCTCCGAGAGCGAGAGGAGTGG 1503  
Qy 1639 TGTGCAATTAACCTGCCCCAGGAGTGTCACTGTGTCGCCGCTGTGAGCTGTGCTGATGCT 1698  
Db 1504 TGTGCAATTAACCTGCCCCAGGAGTGTCACTGTGTCGCCGCTGTGAGCTGTGCTGATGCT 1563  
Qy 1699 ATTTTGGGAGCCCTTGGGGAGAGCTGCCCCCAAGTGAAGGCTTTGTCAAGCCCTGTCAATGCA 1738  
Db 1564 ACTTTGGGAGCCCTTGGGGAGAGCTGCCCCCAAGTGAAGGCTTTGTCAAGCCCTGTCAATGCA 1623  
Qy 1759 ACAACAAGTGAAGCTGAGTCTCCGAGAACTGAGACCGCTGACAGAGAGGAGTGTGA 1818  
Db 1624 ACAACAAGTGAAGCTGAGTCTCCGAGAACTGAGACCGCTGACAGAGAGGAGTGTGA 1683  
Qy 1819 AGTGCATCCACACAGACAGCTGGGGTCCACTGTGACCACTGCAAAAGCAGGCTACTATGAGG 1878  
Db 1684 AGTGCATCCACACAGACAGCTGGGGTCCACTGTGACCACTGCAAAAGCAGGCTACTATGAGG 1743  
Qy 1879 ACCCGTTGGCTCCCAATCCACAGACAGAGTGTGAGCTTGTCAAGCTGCAAGCCAGTGGGCT 1938  
Db 1744 ACCCATTTGGCTCCCAATCCACAGACAGAGTGTGAGCTTGTCAAGCTGCAAGCCAGTGGGCT 1803  
Qy 1939 CGAGAGCTGTGAGAGTGTGAGAGTGTGAGAGCTGTTTGAAGCGAGGCTTTGGTGGCC 1998  
Db 1804 CAGAGCTGTGAGAGTGTGAGAGTGTGAGAGCTGTTTGAAGCGAGGATTTGGTGGCC 1863  
Qy 1999 TCAGCTGTGAGAGTGTGAGAGCTGCAAGCTGCTCAAGCTTGTATTAATCAAGTGAAGTTTC 2058  
Db 1864 CCAACTGTGAGAGTGTGAGAGCTTGTATTAATCAAGTGAAGTTC 1920  
Qy 2059 AGATGATCAATTTATGAGAGCTCCAGATCTGAGAGGCTGATTTTGAAGGCTCAGG 2118  
Db 1921 AGATGATCAATTTATGAGAGCTTCAAGAAATGAGAGGCTGATTTTCAAGAGGCTCAGG 1980

Qy 2119 G-----TGAGCAGTACCCAGACGAGAGCTGGAAGGAGAGATCAGAGGCTGAGCAGG 2172  
Db 1981 GTGAGTATGAGAGTATGATCTATACAGAGCTGGAAGGAGAGATCAGAGGCTGAGCAGG 2040  
Qy 2173 CCCTTGGGAGATTTCTGAGAGAGCCAGATTTCAAGATGCTGTTAGATCTTCAATC 2232  
Db 2041 CCCTTGGGAGATTTCTGAGAGATTTCCAGATTTGAGAGGCTGAGAGATCTTCCCTGGTC 2100  
Qy 2233 TCGGGGTGGCCAAAGGAGCTCAAGAGATTAATCTACCGGAGAGGCTGGATGAGCCCA 2292  
Db 2101 TCCAGTTGGCCAAAGGAGGAGCCAAAGAGACACTACAGAGCGCTGGATGAGCTCA 2160  
Qy 2293 AGATGATGTTGGAAGAGATTTGGGCTGAGGCTGAGTATCAAGACCAATGATGAGATA 2352  
Db 2161 AGATGATGTTGGAAGAGATTTGGGCTGAGGCTGAGTATCAAGACCAATGATGAGATA 2220  
Qy 2353 CTGCGAGCTCATCTCAGATGCGCTGAGCTGAGGAGAAAGTGAAGCTTCCCTGCAAA 2412  
Db 2221 CTCACAGGCTCATCTCAGATGCGCTGAGCTGAGGAGAAAGTGAAGCTTCCCTGCAAA 2280  
Qy 2413 ACACCAATTCCTCTTCAAGAGATTAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2472  
Db 2281 ACATTAATTCCTCTTCAAGAGATTAATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2340  
Qy 2473 AGAGAGCCAGAGATTTGAGAGAGCCATGTTCACTAGTACAGCCAGTGAAGAGCACTGG 2532  
Db 2341 AGAGAGCCAGAGATTTGAGAGAGCCATGTTCACTAGTACAGCCAGTGAAGAGCACTGG 2400  
Qy 2533 CAAAGGAAACCCAGAGATTTCAAGAGATGATGATCACTGTTGCGGAGGCTTGCAGG 2592  
Db 2401 CAAAGGAAACCCAGAGATTTCAAGAGATGATGATCACTGTTGCGGAGGCTTGCAGG 2460  
Qy 2593 AAGAG-----GGGAAAGCGGAGCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2646  
Db 2461 AAGAGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2520  
Qy 2647 AATGCAAGAACTAAATCTTGGCCAGAGGAGTGTGAGAGGAGGAGGAGGAGGAGGAGG 2706  
Db 2521 AATGCAAGAACTAAATCTTGGCCAGAGGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGG 2580  
Qy 2707 TGAAGCAGATAGGCTTATCAGATAGTCTCAACCTTCTCAATTCGCTGTCTAGATTC 2766  
Db 2581 TGAAGCAGATAGGCTTATCAGATAGTCTCAACCTTCTCAATTCGCTGTCTAGATTC 2640  
Qy 2767 AGGAGTCAATGATCAGTCTTGAAGT--AGAGCAAGAGAGGCTGAGAGAGGAGGAGG 2823  
Db 2641 AGGAGTCAATGATCAGTCTTGAAGT--AGAGCAAGAGAGGCTGAGAGAGGAGGAGGAGG 2700  
Qy 2824 ATTCCTCTCAAAACCGTGTGACTAAGCATATGATGATGATGATGATGATGATGATGATG 2883  
Db 2701 ATTCCTCTCAAAACCGTGTGACTAAGCATATGATGATGATGATGATGATGATGATGATG 2760  
Qy 2884 TGGGAACTGGGAAAGAAACCCGAGCTTTTACAGATGAGAGAGGAGGAGGAGGAGGAGG 2943  
Db 2761 TGGGAACTGGGAAAGAAACCCGAGCTTTTACAGATGAGAGAGGAGGAGGAGGAGGAGG 2820  
Qy 2944 CATCAGATCAGCTCTTCCCGTGCACACTTGTCTTAAAGAGAGAGGAGGAGGAGGAGGAGG 3003  
Db 2821 AATCAGATCAGCTCTTCCCGTGCACACTTGTCTTAAAGAGAGGAGGAGGAGGAGGAGG 2880  
Qy 3004 GTATGGCAATGGCACTTTTATGAAGTGTGAACATCTTAAAGATCTGAGAGATTTG 3063  
Db 2881 GTATGGCAATGGCACTTTTATGAAGTGTGAACATCTTAAAGATCTGAGAGATTTG 2940  
Qy 3064 ACTGCAAGTGTGAGATTAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3123  
Db 2941 ACTGCAAGTGTGAGATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3000  
Qy 3124 TCAGCCAGAGGTTGAGAGTCCAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3183  
Db 3001 TCAGCCAGAGGTTGAGAGTCCAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3060





OY	799	ACTACAGTGTCCATPAATAATCCTCTCCCTTCATCAAGATGTTGATGCGTGGAAAGCGTG	858
Db	667	AATACAGTGTCCATPAATAATCACCCTCTACCTTTCTCAAGATGTTGATGCGTGGAAAGCGTG	726
OY	859	TCCAAAGAAAGCGGCTCTCCGCAAAAGTCCAGTGCATACAGCGCATCGGGATATATATTA	918
Db	727	TCCAAAGAAAGGCTCTCTCCGCAAAAGTCCAAATGTTACAGCGCATCAAGATGTTTA	786
OY	919	GCTCAGCAGCAGCATCAGACCCCTGTCTATTTTGTAGTCCCTGGCAAAATTTCTTGGGATTC	978
Db	787	GCTCAGGCCAACAGCACTAGACCCCTGTCTATTTTGTGGCTCCTGGCAAAATTTCTTGGGATTC	846
OY	979	AACAGGTGAGCTACGGGCAAAAGCTATCTTTTGACTACCGTGTGTGATAGGGAGAGCAGAC	1038
Db	847	AACAGGTGAGCTATGGCTCAAAGCCCTGTCTTTGACTACCGTGTGTGACAGAGAGAGCAGAC	906
OY	1039	ACCATATCGCCATGATGATGATCCCTGGAAGTGGCTGTGCTACGGATACAGACATCCCTCTGA	1098
Db	907	ACCATATCGCCATGATGATGATTTCTGGAAGTGGCTGTGCTACGGATACAGACATCCCTCTGA	966
OY	1099	TGCCACTTTAGCAGACACTGCGCTTGTGGATCACCAGACTTACCACTTACAGTTAAGT	1158
Db	967	TGCCACTTTGGCAGAACACTGCGCTTGTGGATCACCAGACTTACCACTTACAGTTAAGT	1026
OY	1159	AACATTCAGAGATTAATTTGGAGCCCGCCAGCTAAAGTTACTTTGATGATCGAGAGGTTACTGC	1218
Db	1027	AGCATTCAGAGCAATTAATTTGGAGCCCGCCAGCTAAAGTTACTTTGATGATCGAGAGGTTACTGC	1086
OY	1219	GGAACCTTCACAGCCCTCGGATCCGAGCTACTACGGAGATAATCAGTACHTGGGTACATTTG	1278
Db	1087	GGATCTTCACAGCCCTCGGATCCGAGCTACTATGTAGAGATAATCAGTACHTGGGTACATTTG	1146
OY	1279	ACAACGTGACCTTATTTTCAAGCCCGCCGTTTGTGAGAGCCCGACGCCCTCGGGTTAATC	1338
Db	1147	ACAATGTGACCTTATTTTCAAGCCCGCCGCTGTCTGTGAGAGCCCGACGCCCTCGGGTTAATC	1206
OY	1339	AATGTGTATGCGCCCTGTGGGTACACAAGGGGCGAGTTCTCCAGAGATTGTGCTCCGGCTACA	1398
Db	1207	AGTGTATATGTCTGTTGGGTACACAAGGGGCGAATTTCTCCAGAGATTGTGCTTGTGCTACACA	1266
OY	1399	AAGAGATATCACCCAGACTGGGACCTTTTGGACCTGTATTCATGTATCTGCCAAGGGG	1458
Db	1267	AGAAGATATTCAGCCAGACTGGGACCTTTTGGACCTGTATTCATGTATCTGCCAAGGGG	1326
OY	1459	GAGGGGCGCTGGATTCAGACACAGAGAGACGTTCCTCAGGGGAGTAACCCCTACATCC	1518
Db	1327	GAGGGGCGCTGTGATTCACACAGAGAGATTTTATTCAGGGGAGTAACATCTGTACAT--	1384
OY	1519	CTGAGTGTCTGATGCGCCCATTTGGTTTCTACAACGATTCACACAAGACCCCGCAGCTGCA	1578
Db	1385	-TGAGTGTGTCTGATGCGCCCATTTGGTTTCTACAACGATTCGACAGACCCCGCAGCTGCA	1443
OY	1579	AGCGGTGCGCCCTGTGCGAATGGGTTCAGACGTCTCCGATGATGCCCTGADACAGAGAGAGTTGG	1638
Db	1444	AGCGATGTCTCTGTATPACGGGTTTCAGCTGTCTCAGTGTATCCCGGAACGGAGAGGTTGG	1503
OY	1639	TGTCCAAATTAATGCGCCCGCAGGGGTCTACTGTGTGCCCTGTGAGCTCTGTGTCTATGGCT	1698
Db	1504	TGTCCAAATTAATGCGCCCTCCGGGGTCAACCGGTGTGCCCTGTGTAGCTCTGTGTATGGCT	1563
OY	1699	ATTTTGGGGACCCCTTGGGGACAGTGTGCCCATGTGAGGCTTTGTACGCTCTGTCAATGTCA	1758
Db	1564	ACTTTGGGGACCCCTTGTGTGTAAATATGGCCCGACAGAGAGCCCTTGTACACCCCTGTCAATGTCA	1623
OY	1759	ACAACAACGTGGACCTTGTGCTCTCCGGAAGTCTTGACCCGCTACACAGGCGAGGTGTCTGA	1818
Db	1624	ACAACAATGTGGACCCCATGTGCTCTCTGGGAATTTGTACCCGCTCTACAGCAGAGGTGTTGA	1683
OY	1819	AGTGCATTCACACAACAGTGGGTTCACCTGTGACCAAGTGCAAAAGCGCTACTATGTGGG	1878
Db	1684	AGTGTATTCACACAACAGCGCGCATTTACTCTGACACAGTGCAAAAGCGCTACTATGTGGG	1743

QY	1879	ACCCTTGTCCTCCAAATCCAGACAGACAAGTGTGAGCTTGCACCTGCAACCCAGTGGCT	1938
Db	1744	ACCCATTTTGGCTCCCAACCCAGACACAAGTGTGAGCTTGCACCTGCAACCCAGTGGCT	1803
QY	1939	CGAGAGCCGTGTGAGTGTGCAAGTGTATGGACGTGTGTTTGCAGAGCCAGGCTTGTGTGGCC	1998
Db	1804	CAGAGCCTGTAGATGTGTGAGAGTATGGACCTGTGTGTTGCAGAGCCAGGATTTGTGTGCC	1863
QY	1999	TCAGCTGTGACATCGCGACACTGACAGCTGTCCAGCTTGTCTTAATCAAGTGAAGTTTC	2058
Db	1864	CCAACGTGACATGAGACATTT---CAGCTGTCCAGCTTGTCTTAATCAAGTGAAGTTTC	1920
QY	2059	AGATGGATCACTTTATGCAGAGACTCCAGATCCTGGAGGCCCTGATTTGCAGAGCTCAGG	2118
Db	1921	AGATGGATCACTTTATGCAGAGACTCCAGATCCTGGAGGCCCTGATTTGCAGAGCTCAGG	1980
QY	2119	G-----TGAGACAGTACCCAAACCAGAGCTGGAAGGACAGATGACAGACGCTGAGCAGG	2172
Db	1981	GTGGTGAATGAGTAGTATGTAACCTGATACAGAGCTGGAAGGACAGATGACAGACGCTGAGCAGG	2040
QY	2173	CCCTTCGGGACATTTCTGAGAGAACCCAGATTTTACAAGATGCTGTTAATCCTTCAATC	2232
Db	2041	CCCTTCAGAGACATTTCTGAGAGATCCCAAGATTTGAGAAGGTGCTAGACAGATCCCTTGTC	2100
QY	2233	TCGGAGTGTCCAAAGCACAAGCTCAAGAAATAGCTACCGGAGACCGCTGATGACCTCA	2292
Db	2101	TCAGATGTGGCCAGAGTGAAGAGCCAAAGAAAGACCTACAGAGCCGCTGTGATACCTCA	2160
QY	2293	AGATGACTGTGAAAAGAGTTGCGGCCCTTGGGACGTACGATCAGAACCAAGTTCCAGATA	2352
Db	2161	AGATGACTGTGAAAAGAGTTGCGGCCCTTGGGAAATGCTACGTAACCAAGCTGATGCGATA	2220
QY	2353	CTCGAGGCTCATACATCAGATGTGGCCGTGAGGCCCTGAGAGAAAGTGAAGCTTCCCTGAAA	2412
Db	2221	CTCGAGGCTCATACATCAGATGTGGCCGTGAGGCCCTGAGAGAAAGTGAAGCTTCCCTGAAA	2280
QY	2413	ACACCAATTTCTCCTTCAGAGACACTACGTGGGGCCCAAAATGCTTTAAAAGTGTGGCTC	2472
Db	2281	ACACTAACTTCTGCGCTCAGAACCACTACGTGGGGCCCAAAATGCTTTAAAAGTGTGGCTC	2340
QY	2473	AGGAGGCCACAGATTTGGCAGACAGCCATGTTCACTAGTACAGCAGTAATGTAGAGCACTGG	2532
Db	2341	AGGAGGCCACAGATTTAGCAGAAAGCCACGTTGAGTACAGCCAGTAATGTAGAGCACTGA	2400
QY	2533	CAAGAGAAACCCAGAGATTTCCAAAGAGCTGATGTCACTGTGTGCGAGGCTGTGAGG	2592
Db	2401	CAAGAGAAACCTGAGAGACTATTCCAAACAGCCCTCTCACTGTGTGCGAGGCTGTGATG	2460
QY	2593	AAGGAG-----GCGGAAGCGGCGAGCCTGAGCGAGCCGTGTGTCAAAAGGCTTGTGGAA	2646
Db	2461	AAGGAGTGTGGAAGGGAAGCGGTGAGCCGCGAGCGGTGTGTGTGTCAAAGGAGCTTGTGGAA	2520
QY	2647	AATTGCAAAAATTAATCTCTGGGCCAGAGTTGTGAGAGGAGGCCACGCAACCCACA	2706
Db	2521	AATTGAGAAAAACCAAGTCCCTGTGGCCACAGACTTGACAAAGGGAAGGCCACTCAAGCGAAA	2580
QY	2707	TGGAAGCAGATAGGCTTTATCAGCATAGTCTCCACCTTCTCAATTCGCTGTCTCAGATTC	2766
Db	2581	TTGAAGCAGATAGGCTTTATCAGCATAGTCTCCACCTTCTCAATTCGCTGTCTCAGATTC	2640
QY	2767	AGGAGCTAAATGATCAGTCTTTCGACG---AGAAAGGAAGAGGCTCAGACAAAACCTG	2823
Db	2641	AGGAGTATGATATAGTCTTTCGACGGTGGAAGGAAGCAAAAGGATCAACAAAAAGGGG	2700
QY	2824	ATTCTCTCTCAAAACGCTGTGACTAAGCATATGATGTAATTCGTAACAGCTGCAAAAGCATC	2883
Db	2701	ATTCTCTCTCAAGCCTGTGTAAACAGGCATATGATGTAATTCGTAACAGCAAGATATC	2760
QY	2884	TGGGAACCTGGGAAGAGAAGAAACCCGGCAGCTTTACAGATATGGAAGAAATGTGGAGACAGA	2943
Db	2761	TGGGAACCTGGGAAGAGAAGAAACACAGCAAGCTTTACAGAAATGGAAGAAATGTGGAGAGAGA	2820
QY	2944	CATCAGATCAGCTGCTTCCGCTGCAACCTTGTCTAAAAGCAGAGGCCAAGACACACTAA	3003



Db 448 CAACTGATGCTGTACCCAGCTGCATCGCAGGGCCCTGTGACGGGCCCTGTGCTG 507  
Qy 668 CAAACCCGGCTGTGCTGAGAGCGCTGTGATAGGTGTGACAGGATTAATCACTGGA 727  
Db 508 CAAACCCAGCTGTGCTGAGAGCGCTGTGATGAGGTGTGATCAATTAATCTGGA 567  
Qy 728 TGGGGGAAACCCCTGAGGGCTGTACCAAGTGTGTTTGTGATGGGATTCCGGCAGCTGCA 787  
Db 568 TGGGGGGAACCCCTGAGGGCTGTACCAAGTGTGTTTGTGATGGGATTCCGGCAGCTGCG 627  
Qy 788 CAGCTGTGGGACTACAGTGTCCATAAATCATCTGCTTCATCAAGATGTTGATG 847  
Db 628 CAGCTGTGAGAAATACAGTGTCCATAAATCATCTTCATCAAGATGTTGATG 687  
Qy 848 CTGGAAGGCTGTCCAAAGAAACGGGTCTCTGCAAGCTCCAGTGTGACAGCCCATCG 907  
Db 688 CTGGAAGGCTGTCCAAAGAAATGGGTCTCTGCAAGCTCCAAATGTCACAGCCCATCA 747  
Qy 908 GGATATATTTAGCTACAGCAGCAGATCAGACCTGTCTATTTTGTAGCTCCGCAATT 967  
Db 748 AGATGTGTTAGCTACAGCCACAGACTAGACCTGTCTATTTTGTGGCTCCTGCCAATT 807  
Qy 968 TCTTGGAAATCAACAGGTGAGCTACGGGCAAAAGCTATCTTTGACTACCGTGTGATG 1027  
Db 808 TCTTGGAAATCAACAGGTGAGCTATGGGCAAAAGCTGTCTTGTACTACCGTGTGACAG 867  
Qy 1028 GGGGAGGAGACACCATCTGCCCCATGACGTGATCTCGAAGAGTCTGCTACAGGATCAC 1087  
Db 868 AGGAGGAGACACCATCTGCCCATGATGATCTCGAAGGTCTGCTGTACAGGATCAC 927  
Qy 1088 AGCTCCCTGTGATGCTACAGCAGACACTGCTTGTGGATCACAAGACTTACACTT 1147  
Db 928 AGCTCCCTGTGATGCTACAGCAGACACTGCTTGTGGATCACAAGACTTACACTT 987  
Qy 1148 CAGATTAAATGACATCCAAAGCAGTAATGGAGCCCCCAGCTAAAGTTACTTTGAGTATCG 1207  
Db 988 CAGATTAAATGAGCATCCAAAGCAGTAATGGAGCCCCCAGCTAAAGTTACTTTGAGTATCG 1047  
Qy 1208 GAGTTTCTGGGGAACCTCAACAGCCCTGGCGATCCGAGCTACCTACAGGAAATACAGTAC 1267  
Db 1048 AAGTTTCTGGGGAATCTCAACAGCCCTGGCATCCGAGCTACATATGAGAAATACAGTAC 1107  
Qy 1268 TGGGTACATTGACAAAGCTGACCTGTGATTTAGCCCGCCGCTTCTGGAGCCCCAGCGCC 1327  
Db 1108 TGGGTACATTGACAAAGCTGACCTGTGATTTAGCCCGCCGCTTCTGGAGCCCCAGCGCC 1167  
Qy 1328 CTGGGTTGACAAATGTTGATGCCCTGTGGCTACAAAGGGCAGTTCTGCGAGATTGTC 1387  
Db 1168 CTGGGTTGACAAAGTTGATGTTGCTGTGGGTACAAAGGGCAGTAATCTGCGAGATTGTC 1227  
Qy 1388 TTCCGGGTACAAAGAGATTCAGCAGACTGGGACCTTTGGACCTGTATTCATGTA 1447  
Db 1228 TTCTGGGTACAAAGAGATTCAGCAGACTGGGACCTTTGGACCTGTATTCATGTA 1287  
Qy 1448 CTGCGAAGGGGAGGGGCTGCGATCCAGACAGAGAGACTGTACTACAGGGATGAGAA 1507  
Db 1288 CTGCGAAGGGGAGGGGCTGCGATCCAGACAGAGAGATGTATTCAGGGGATGAGAA 1347  
Qy 1508 CCTGACATCCCTGATGTGTGCTGACGTGCCCATTTGTTTCAACGATCCACAAGACC 1567  
Db 1348 TCTGACAT--TGAAGTGTGCTGACTGCCCAATTGGTTTCAACGATCCGACGACC 1404  
Qy 1568 CCGAGGTGCAAGCGCGTCCCTGTGCAATAGGGTTGACGTGCTCCGATGATGCTGAGAC 1627  
Db 1405 CCGAGGTGCAAGCGCGATGCTCTGTCAATAGCGGTTGACGTGCTCAAGGATGCGGAGAT 1464  
Qy 1628 AGAGAGGTGTGTGCAATAACTGCCCAAGAGTGTACTGTCGCCGCTGTGAGCTGTG 1687  
Db 1465 GGAAGAGGTGTGTGCAATAACTGCCCGGGGTGACCGGTCGCCGCTGTGAGCTGTG 1524  
Qy 1688 TGCTGATGCTATTTTGGGGACCCCTTGGGGGAAGTGTGCCAGTGAAGCCCTTGTGAGCC 1747  
|||||

Db 1525 TGCTGATGCTACTTTGGGGACCCCTTGTGTGAACATGCCCCAGAGGACCTGTGAGCC 1584  
Qy 1748 CTGTGAGTGCACAAACAAACGTGAGACCTAGTGTCTCCGGGAACGTGTGACCCCTGACAGG 1807  
Db 1585 CTGTCAAGTGCACAAACAAATGTGAGACCCAGTGTCTGGGAATGTGTGACCCGGTGTGACG 1644  
Qy 1808 CAGGTGTGAAAGTGCATCCACAAACAGCAGCTGGGGGTGCACATGTACCCAGTCAAGAGCAG 1867  
Db 1645 CAGGTGTGAAAGTGTATCCACAAACAGCCGGGATCTACTGTGACACAGTCAAGAGCAGG 1704  
Qy 1868 CTACTAGGGGACCCGTTGGCTCCCATTCAGCAGACAGATGTGTGAGCTTGCACATGCA 1927  
Db 1705 CTACTGTGGGAGCCCATTTGGCTCCCAACCCAGCAGACAGATGTGTGAGCTTGCACATG 1764  
Qy 1928 CCCAGTGGGCTGAGAGCTGTGAGAGTGTGCAAGATGTGAGCAGTGTGTTTCCAGCCAGG 1987  
Db 1765 CCCAGTGGGCTGAGAGCTGTGAGAGTGTGCAAGATGTGAGCAGTGTGTTTCCAGCCAGG 1824  
Qy 1988 CTTTGTGGCTGTGAGCTGTGAGAGTGTGAGAGCTGTGAGAGCTGTGATTAATCA 2047  
Db 1825 ATTTGTGGCCCCCAACTGTGTGAGATGAGCAATT--CAGCTGTCCAGCTTCTATTAATCA 1881  
Qy 2048 AGTGAAGTTCAGATGATGATCATGTTATGACAGCAGCTCCAGATTCGTGAAGCCGTGATTC 2107  
Db 1882 AGTGAAGATTCAGATGATGATCATGTTATGACAGCAGCTTCAGAGAAATGAGGCCCTGATTC 1941  
Qy 2108 GAAAGCTCAGGG-----TGAGCAGATCCCAACGAGAGCTGTGAAGGACAGATGACCA 2161  
Db 1942 AAGAGCTCAGGGGTGTGATGAGATGATCATGATTAACAGATGTGAAGGACAGATGACCA 2001  
Qy 2162 GCGTGAAGAGCCCTTGGGACATTCGTGAGAGAGCCAGATTCACAAAGATGCTGTTAG 2221  
Db 2002 GCGTGAAGAGCCCTTGAAGACATTCGTGAGAGATGCCAGATTCAGAGAGTGTCTAGAG 2061  
Qy 2222 ATCTTCAATCTCCGGGTGCGCAAGGAGACTCAAGAGATTAAGTACCGGACCGCT 2281  
Db 2062 ATCTTGTGTCTCCAGTTGCGCAAGTGTGAGAGGACCAAGAAACAGCTACAGACCGCT 2121  
Qy 2282 GGATGACCTCAAGATGATGTGAAAGATGTCGGCCCTGGGAGTCAATTCAGAAACCA 2341  
Db 2122 GGATGACCTCAAGATGATGTGAAAGATGTCGGCCCTGGGAGTCAATTCAGAAACCA 2181  
Qy 2342 AGTTCAGATTCCTGCGAGGCTCATCATCAGATGCGCTGAGCTGTGAGAGAGTGAAGC 2401  
Db 2182 AGTTCAGATTCCTGCGAGGCTCATCATCAGATGAGTGTGAGCTGTGAGAGAGTGAAGC 2241  
Qy 2402 TTCCCTGCAAAACCAACATTCCTCTTCAAGACACTAGTGGGGCCAAATGGCTTAA 2461  
Db 2242 TTCCCTGGAAGAACATTAATTCCTGCTCAGACCACTAGCTGGGGCCAAATGGCTTAA 2301  
Qy 2462 AAGTCTGGCTGAGAGGCGCAGATGTGGCAGACAGCCATGTGATGAGCCAGTAAAT 2521  
Db 2302 AAGTCTGGCTGAGAGGCGCAGATGTGAGAAAGCCAGCTGTGATGAGCCAGTAAAT 2361  
Qy 2522 GGAGCACTGTGCAAAAGAAACCCAGAGATTTCCAAAGCTGATGTCTACGTGTGCGGA 2581  
Db 2362 GGAGCACTGTGCAAAAGGAAATAGAGATTTCCAAAGCCCTCTACGTGTGCGGA 2421  
Qy 2582 GGCCTGTGAGGAGAG-----GCGGAGCGGACGCTGTGAGCGAGCCGTTGTCAAG 2635  
Db 2422 GGCCTGTGAGGAGAGTGTGAGAGCGGAGTGTGAGCGAGCGTGTGTGTGAGCAAG 2481  
Qy 2636 GCTTGTGGGAAATTTGCAAGAACTTAATCTCTGCGCCAGAGATTTGTGAGGAGGCGAC 2695  
Db 2482 GCTTGTGGGAAATTTGCAAGAAACCAAGTCTCTGCGCCAGAGTGTGAGCAAGGAGGCGAC 2541  
Qy 2696 GCAAGCAGCATGTGAGAGATGATGCTTATCAGCATATGTTCCACCTTGTCAATTCCT 2755  
Db 2542 TCAAGCAGAAATTTGAGCAGATAGTGTATATCAGCAGATGTCCGCTCTGTGATGAT 2601  
Qy 2756 GTCTCAGATTCAGGAGTCAATGATCAGTCTTTCAGGT--AGAAGGAGAGGCTTCAG 2812  
Db 2602 GTCTCAGTTCAGGAGTCAATGATCAGTCTTTCAGGTGAGAGAGGAGATTCAG 2661  
|||||

QY 2813 ACAAAAGCTGATTTCTCTCAAAACGCTGTGACTAAGCATATGATGATTCAGACAGCT 2872  
 Db 2662 ACAAAAAGCGATTCACCTCTCAAGCCTGTGTATACCAAGCATATGATGATTCAGACAGCT 2721  
 QY 2873 GCAAAAGCATCTGGGAAACTGGGAAAGAAACCCGCGAGCTCTTACAGATGGAAGAA 2932  
 Db 2722 ACAAAAGAAATCTGGGAAACTGGGAAAGAAACACACACTCTCTTACAGATGGAAGAA 2781  
 QY 2933 TGGGAGACAGCATCATGATGATGCTTCCCGTGGCAACCTTGTCTTAAAGCAGAGCCA 2992  
 Db 2782 TGGGAGAGAGAAATCATATCACTGCTTCCCGTGGCAATCTGTCTTAAAGCAGAGACA 2841  
 QY 2993 AGAAGCACTAAGTATGGGCAATGCGACCTTTTATGAAGTTGAGAATCTTAAAGATCT 3052  
 Db 2842 AGAAGCACTGATGATGGGCAATGCGACCTTTTATGAAGTTGAGAATCTTAAAGATCT 2901  
 QY 3053 CAGAGATTTGAGCTGAGTGGAGATTAAGAGCAAGACTGTAAGAGCCATGAAGAG 3112  
 Db 2902 CAGAGATTTGAGCTGAGTGGAGATTAAGAGCAAGACTGTAAGAGCCATGAAGAG 2961  
 QY 3113 ACTCTCTACATCAGCCAGAAAGTTTGAGGTGCGAGTGCAGACAGAGCAAGAGCAAGAG 3172  
 Db 2962 ACTCTCTACATCAGCCAGAAAGTTTGAGGTGCGAGTGCAGACAGAGCAAGAGCAAGAG 3021  
 QY 3173 AGCCCTGGGAGTGTCTGCTGCCAGCCAGAGGCAAAAGATGCAAGCCAGAGGAGCCCT 3232  
 Db 3022 AGCCCTGGGAGTGTCTGCTGCCAGCCAGAGGCAAAAGATGCGAGGAGGAGCCCT 3081  
 QY 3233 GGAGATCTCTGGCAAGTATACAGAGAGATAGAGAGTCTGACCTGAGACCAATGTGAC 3292  
 Db 3082 GGAATCTCCAGTAGAGATTAACAGAGAGATGGAGATTCGTAACCTGGAACCAATGTGAC 3141  
 QY 3293 AGCAGATGAGACCTTGGCCATGTGAGAGAGACTGGCCACTGTGAAAGTGAAGATGAGAG 3352  
 Db 3142 AGCAGATGAGACCTTGGCCATGTGAGAGAGACTGGCCACTGTGAAAGTGAAGATGAGAG 3201  
 QY 3353 AGTGAAGAGAGCTGTCAAGAGAGAGAGAGAGAGTTTGACATGATATGAGACGCAATGCA 3412  
 Db 3202 AGTGAAGAGAGCTGTCAAGAGAGAGAGAGAGAGTTTGACATGATATGAGACGCAATGCA 3261  
 QY 3413 GATGATTAATTCAGAGAGCCCAAGAGAGTTGAAACAGAGCCCAAGATCTGTGATGATGAT 3472  
 Db 3262 GATGATTAATTCAGAGAGCCCAAGAGAGTTGATACAGAGCCCAAGATCTGTGATGATGAT 3321  
 QY 3473 CCAAGACACACTCAACACTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 3532  
 Db 3322 CCAAGACACACTCAACACTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 3381  
 QY 3533 GGATGAAGAGAGCTGTCTTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3592  
 Db 3382 AGATGAAGAGAGAGCTGTCTTACTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3441  
 QY 3593 CAGGAG 3652  
 Db 3442 CAGGAG 3501  
 QY 3653 CCTCCGTTTCTGTGAG 3712  
 Db 3502 CCTCCGTTTCTGTGAG 3561  
 QY 3713 CATCAGGAG 3772  
 Db 3562 CATCAGGAG 3621  
 QY 3773 CTGCGTTAGAGATTTCTCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3832  
 Db 3622 CTGCGTTAGAGATTTCTCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 3681  
 QY 3833 TCTCA 3837  
 Db 3682 TGTCA 3686

RESULT 7  
 AA224627  
 ID AA224627 standard; cDNA; 5152 BP.  
 XX  
 AC AA224627;  
 XX  
 DT 07-DEC-1999 (first entry)  
 XX  
 DE Human lung tumor associated polynucleotide.  
 XX  
 KW Human; lung tumor; lung cancer; T cell stimulation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W09947674-A2.  
 XX  
 PD 23-SEP-1999.  
 XX  
 PE 17-MAR-1999; 99WO-US05798.  
 XX  
 PR 18-MAR-1998; 98US-0040802.  
 PR 18-MAR-1998; 98US-0040984.  
 PR 27-JUL-1998; 98US-0123912.  
 PR 27-JUL-1998; 98US-0123933.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Reed SG, Wang T;  
 XX  
 DR WPI: 1999-571839/48.  
 XX  
 PT New isolated lung tumor polynucleotides, used to develop products for  
 PT the treatment, prevention and monitoring the progression of lung cancer  
 PT  
 PS Claim 12; Page 119-120; 148pp; English.  
 XX  
 CC The invention provides isolated human lung tumor nucleic acids and  
 CC polypeptides. The polypeptides can be used for the treatment of lung  
 CC cancer. The polypeptides and polynucleotides can be used to stimulate T  
 CC cells or antigen presenting cells for use in the treatment of lung  
 CC cancer. The polypeptides and monoclonal antibodies specific for the  
 CC polypeptides can also be used to inhibit the development of lung cancer.  
 CC Agents which bind the polypeptides can be used for detecting lung cancer  
 CC and for monitoring the progression of lung cancer.  
 XX  
 SQ Sequence 5152 BP; 1351 A; 1221 C; 1377 G; 1203 T; 0 other;  
 Query Match 72.9%; Score 2908.4; DB 20; Length 5152;  
 Best Local Similarity 88.3%; Pred. No. 0;  
 Matches 3281; Conservative 0; Mismatches 401; Indels 32; Gaps 10;  
 QY 146 CAGAGGCGCGGAG 138  
 Db 7 CGAGGCGCGGAG 66  
 QY 199 TGCCTGGGCTGTGAG 258  
 Db 67 TGCCTGGGCTGTGAG 126  
 QY 259 CCACTTCGAG 318  
 Db 127 CCACTTCGAG 186  
 QY 319 AGAAGCTTCAG 378  
 Db 187 GGAAGCTTCAG 246  
 QY 379 ATGAGCATCCAGCTGAG 438  
 Db 247 ATGAGCATCCAGCTGAG 306

QY	439	GTTTACCCCTGCAATTGTTAACCTTAAGGTTCTCTTAAGCCTCGATGTGACAACTCTGAC	498
Db	307	GTTTGCCCTGCAATTGTTAACCTCCAAAGTTCTCTTAAGTGGCTCGATGTGACAACTCCGAC	366
QY	499	GGTCAGCTGTAAACCCAGGTGTGACAGAGACAGGTGTGACCCGATGTCTCCCGGGCTCC	558
Db	367	GGTCAGCTGTAAACCCAGGTGTGACAGAGACAGATCGAACCGATGTCTCCAGGGCTCC	426
QY	559	ACACACTCACTGATGCTGGGTGCGCCCAAGACCAAAAGCTGCTAGACTCCAAAGTGTGACT	618
Db	427	ACATGTCTACGGGATGGGGGTGCAACCAAGACCAAGACATGTGATATCCAAAGTGTACT	486
QY	619	GTGACCCACAGCTGCATCTCAGGGCCCTGTGTACTAGGCCCTGTGTCTGCAAGCCGGCTG	678
Db	487	GTGACCCACAGCTGGCATGTGACAGGGCCC - GTGACCGGGGCCCTGTGTCTGCAAGCCAGCTG	545
QY	679	TCACGTGGAGCGCTGTGATAGGTGTGACACGGTTACTATACCTCGATGGGGGAAAC	738
Db	546	TCACGTGGAGAAAGCTGTGATAGGTGTGATCAGTTACTATACCTGTGATGGGGGAAAC	605
QY	739	CTCAGGCGCTGACCAAGTGTGTTTGTATGAGGCAATTCGCGACAGCTGCACAGCTCTGGG	798
Db	606	CTGAGGGC - GTACCCAGTGTTCGTGCTATGGGCATTTAGCCAGCTGCCCGACCTCTGAC	664
QY	799	ACTACAGTGTCCATAAATCATCTCTGCTCCCTTCATCAAGATGTTGATGGCTGGAAGGCTG	858
Db	665	AATACAGTGTCCATAAAGCTCACTCTCACTTTCATCAAGATGTTGATGGCTGGAAGGCTG	724
QY	859	TCCAAAGAAAGGGGCTCTCTGCAAAAGCTCCAGTGTGTACAGCGCCATCGGGATATATTA	918
Db	725	TCCAAAGAAAGGGGCTCTCTGCAAAAGCTCCAAAGTGTGTACAGCGCCATCAAGATGTGTTTA	784
QY	919	GCTCAGACGACGATCCAGACCCCTGCTATATTGTTAGTCCGACCAATTTCTTGGGAATC	978
Db	785	GCTCAGCCCAAGCACTAGACCCCTGTCTATTTTGTGGCTCTCGCCAATTTCTTGGGAATC	844
QY	979	AACAGGTGTGTACGGGGCAAAAGCCCTATCTTTTGACTACCGTGTGATAGGGGAGCGACAC	1038
Db	845	AACAGGTGTGTATGTGTCAAAGCCCTGTGCTTGTACTACCGTGTGTGACAGAGAGGACGAC	904
QY	1039	ACCATCTGCCCATAGAGTGTATCTGTGAAGGTGCTGGTCTACAGGATACAGACTCCCTTGA	1098
Db	905	ACCATCTGCCCATAGATGTGATTTGTGAAGGTGTGGTGTACAGGATACAGACTCCCTTGA	964
QY	1099	TGCCACTTGAAGACACTGCCCTGTGGGGATCACCAAGACTTACACTTCAGATTATATG	1158
Db	965	TGCCACTTGGCAAGACACTGCCCTGTGGGGCTCACCAAGACTTACACTTCAGATTATATG	1024
QY	1159	AACATCCAAAGCAGTAAATTGGAGCCGCCAGCTAACTTACTTGAGTATTCGAGGTACTGC	1218
Db	1025	AGCATCCAAAGCAATAATTGGAGCCGCCAGCTGATTTACTTGAATATTCGAAGTACTGC	1084
QY	1219	GGAACTTCACAGCCCTGCGGATCCGAGCTACCTACGAGAAATACAGTATGEGTACATYG	1278
Db	1085	GGAAATTCACAGCCCTCGCGATCCGAGCTACATGTGAGATTAACGTAAGTATGGAATCTG	1144
QY	1279	ACAACGTACCTGATTTTCAAGCCGCCGCCCTTCTGAGAGCCCGACGCCCTCGGGTTAAC	1338
Db	1145	ACAATGTACCTGATTTTCAAGCCGCCCTTCTGTCTGGAGCCCGACGCCCTCGGGTTAAC	1204
QY	1339	AATGTGTATGCTCTGTTGGCTACAAAGGGGAGTTCTGCAAGATTGTGCTTCCGGCTACA	1398
Db	1205	AGTGTATATGTCCTGTTGGGTACCAAGGGGCAATCTGCAAGATTGTGCTTCTTGGCTACA	1264
QY	1399	AAAGAGATTTCAGCCAGACTGGGACCTTTTGGCACCTGTATTCCATGTAACTGCCAAGGG	1458
Db	1265	AGAGAGATTTCAGCCAGACTGGGACCTTTTGGCACCTGTATTCTTTTAACTGTCAAGGGG	1324
QY	1459	GAGGGGCTCGGATATCCACACACAGAGAGACTTTTACTCAGGGGATGAGAACCTCTACATCC	1518
Db	1325	GAGGGGCTCGTGTATCCACACACAGAGAGATTTTTATTCAGGGGATGAGAAATCTTACAT -	1382
QY	1519	CTGAGTGTGTGACTGCCCCATTTGGTTTCTACACAGATTCACAGACCCCCCGCAGCTGCA	1578

Db	1383	-TGAGTGTGCTGACGTGCCCAATTTGGTTTCATCAACAGATCCCGACAGACCCCGCAGCTGCA	1441
Qy	1579	AGCCGTGCCCTGTGCGCAATGGGTTCAGACTCTCCGTCATGCTCGAGACAGAGAGAGGTGG	1638
Db	1442	AGCCATGTCTCTGTATACGGGTTTCACTTCTCACTAGTGTATCCCGAGACGGAGAGAGTGG	1501
Qy	1639	TGTGCATTAAGTGCCTCCAGGGGTGTCACTGTGTGCCCGCTGTGTAGCTGTGTCTGATGACT	1698
Db	1502	TGTGCATTAAGTGCCTCCCGGGGTACCGGTGCCCGCTGTGTAGCTGTGTCTGATGACT	1561
Qy	1699	ATTTTGGGGACCCCTTCGGGAGACGTGGCCCAATGAGGCTTGTTCAGCCCTGTCAATGCA	1758
Db	1562	ACTTTGGGGACCCCTTTGGTGAATGTGCCCAATGAGGCTTGTTCAGCCCTGTCAATGCA	1621
Qy	1759	ACAACAAGTGGACCTCTGATGCTCCGGGAAGTGTGAACCGCTGACAGAGGAGGTGTGTA	1818
Db	1622	ACAACAAGTGGACCCAGATGCTCTTGGGAATTGTACCGGCTGTACAGGAGGTGTGTA	1661
Qy	1819	AGTGCATCCACAACACAGCTGGGGTCCACTGTGACCAAGTGCAGAGAGGCTACTATGAGG	1878
Db	1682	AGTGTATCCACAACACAGCCGGCATCTACTGTGACCAAGTGCAGAGAGGCTACTTCCGGG	1741
Qy	1879	ACCGTGTGGCTCCCATTCAGACAGCAAGTGTGCAAGCTTGCACATGCACCCAGTGGCT	1938
Db	1742	ACCCATTTGGCTCCCAACCCAGACAGCAAGTGTGCAAGCTTGCACATGTAAACCCATGGGCT	1801
Qy	1939	CGGAGCCCTGTGACGTGTGGAAGTGTGGACACTGTGTGTGCAAGCCAGGCTTGTGGCC	1998
Db	1802	CAGACCCCTGTGAGATGTGGAAGTGTGGACACTGTGTGTGCAAGCCAGGATTTGGTGGCC	1861
Qy	1999	TCAGCTGTGAGCATCGGCACCTGACAGACACTGTCCAGCTTGCATTAATCAAGTGAAGCTTC	2058
Db	1862	CCAATGTGAGCATGTGAGCATTT--CACTGTCCAGCTTGCATTAATCAAGTGAAGATTC	1918
Qy	2059	AGATGATCAGTTTATGACAGACGCTCCAGATCTTGGAGGCCCTGATTTGCAAGCTCAGG	2118
Db	1919	AGATGATCAGTTTATGACAGACGCTTCAGAGATATGAGAGCCCTGATTTCAAAAGCTCAGG	1978
Qy	2119	G-----TGGAGCAATACCACCAAGCAGAGCTGGGAAGGAGATGACAGAGGCTCAGCAGG	2172
Db	1979	GTTGTGATGAGTAATTAATCTGTAACAGAGCTGGAAGGAGAGATGACAGAGGCTCAGCAGG	2038
Qy	2173	CCCTTCGGGACATTTGTGAGAGAGGCCAGATTTTCAGAGATGCTTGTAGATCTTCATTC	2232
Db	2039	CCCTTCAGAGACA-TCTGAGAGATGCCCCAGATTTTCAGAAAGTGTCTATGCAATGCCCTTGGT-	2096
Qy	2233	TCCGGGTGGCCCAAGGACAGACTCAAGAGAAATAGCTACCGGAGCCGCTGTGATGACTCA	2292
Db	2097	TCCAGTGGGCCCAAGGTGAGAGAGCCAAAGAAACAGCTACCAAGAGCCGCTGTGATGACTCA	2156
Qy	2299	AGATACATGTGGAAGAGTTCGGGCGCTTGGGCAATGCAATATACAGAACCAAGTTCAAGATA	2355
Db	2157	AGATACATGTGGAAGAGTTCGGGCGCTTGGGGAAGTCACTACAGAACCAAGTTCGGGATA	2218
Qy	2353	CTCGAGGCTCATCTCAGATGGCGCTGAGGCTGGAGAAAGTGAAGGCTTCCCGCAAA	2412
Db	2217	CTCAGAGGCTCATCTCAGATGACAGCTGAGGCTTGGCAAGAAAGTGAAGCTTCTTGGAA	2278
Qy	2413	ACACACATTTCTCTTCAGAGCACTACGTGGGGCCAAATGGCTTTAAAGTCTGGCTC	2477
Db	2277	ACACTAACATTTCTCTGCTCAGAGCACTACGTGGGGCCAAATGGCTTTAAAGTCTGGCTC	2336
Qy	2473	AGGAGGCCACGAGATTGGCAGACAGCCATGTTCACTACGCCAGTAACTGTGAGCAACTGG	2533
Db	2337	AGGAGGCCACGAGATTAGCAGAAACCCAGTTGAGTCCGCCAGTAACTGTGAGCAACTGA	2396
Qy	2533	CAAGAGAAACCCAGAGATATCCAAAGAGCTGATGTCACTGGTGGCAGAGGCTGTCCAGG	2592
Db	2397	CAAGAGAAACCTGAGAGCTATTTCCAAACAGCCCTTCACTGTGTGGCAAGGCTGTGCATG	2455
Qy	2593	AAAGAG-----GCGAAGCGGACCTTGAGAGGAGCCGTGGTGCAAAGGCTTGTGGGA	2648

Db 2457 AAGAGTCGAGAGCGGAGCGGTAGCCCCGAGCGTGTGTGTCAGAAAGCGCTGTGTGAAA 2516  
QY 2647 AATTGAGAAAACTAAATCTCTGGCCAGAGATTGTGAGGAGGCGCCAGCAAAACCGACA 2706  
Db 2517 AATTGAGAAAAACCAAGTCCCTGGCCAGAGTTGACAAAGGAGGCGCCACTCAAGCGGAAA 2576  
QY 2707 TGGAGAGATAGTCTTATCAGCATATGTCTCCACCTTCTCAATTCCTGTCTCAGATTTC 2766  
Db 2577 TTGAGAGATAGTCTTATCAGCATATGTCTCCGCTCCGAGATTCAGTCTCTCGGCTTC 2636  
QY 2767 AGGAGATCAATGATCACTCTTCCAGAGT---AGAGAGGAGAGAGCGACAGCAAAAGCTG 2823  
Db 2637 AGGAGATCAATGATCACTCTTCCAGAGATGAGAGAGAGAGAGATCAAAAGAGCGG 2696  
QY 2824 ATTCTCTCTCAAAACCGTGTGACTAAGCATATGATGATGATTCAGACAGCTGCAAGCAATC 2883  
Db 2697 ATTCTCTCTCAAAACCGTGTGACTAAGCATATGATGATGATTCAGACAGCAATC 2756  
QY 2884 TGGGAAATCTGGGAGAGAAACCCGCGAGCTTTACAGAAATGGAAGAAATGGGAGACAGA 2943  
Db 2757 TGGGAAATCTGGGAGAGAAACCCGCGAGCTTTACAGAAATGGAAGAAATGGGAGAGAGA 2816  
QY 2944 CATCATGATCACTGCTTCTCCGTCACCACTTGTCTAAAGCAGAGCGCCAGAGCACTAA 3003  
Db 2817 AATCAGATCACTGCTTCTCCGTCACCACTTGTCTAAAGCAGAGCGCCAGAGCACTAA 2876  
QY 3004 GTATGGGCAATGCCACTTTTATGAAGTTGAGAAATCTTAAAGATCTCAGAGATTTC 3063  
Db 2877 GTATGGGCAATGCCACTTTTATGAAGTTGAGAAATCTTAAAGATCTCAGAGATTTC 2936  
QY 3064 ACCTGCAAGTTGGAGATTAAGAAAGCAGAACTGAAAGGCGCATGAGAGACTCTCTTACA 3123  
Db 2937 ACCTGCAAGTTGGAGATTAAGAAAGCAGAACTGAAAGGCGCATGAGAGACTCTCTTACA 2996  
QY 3124 TCAGCCAGAAAGTTGAGAGTGCAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3183  
Db 2997 TCAGCCAGAAAGTTTCAAGTGCAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3056  
QY 3184 GTCTGCTGCTGCGAGCGCCAGAGGCGCAAGAAATGCAAGCAGAGGCGCCCTGGAATCTCTG 3243  
Db 3057 GCGCTGCTGCTGATGACAGAGAGGCGCAAGAAATGCGGCGGCGGCGCCCTGGAATCTCCA 3116  
QY 3244 GCAAGATAGAAAGAGAGATGAGAGTGTGAATTTGAGAGCCATGTGACAGCAGATGAGAG 3303  
Db 3117 GTGAGATGAAAGAGAGATGAGAGTGTGAATTTGAGAGCCATGTGACAGCAGATGAGAG 3176  
QY 3304 CCTTGGCCATGAG 3363  
Db 3177 CCTTGGCCATGAG 3236  
QY 3364 AGCTGTCAAG 3423  
Db 3237 AGCTGTCAAG 3296  
QY 3424 CAGAGGCGCCAAAGAGTTGAAACAGAGCCAGAAAGTGTGAGAGTACATCAAGACAGACAC 3483  
Db 3297 CAGAGGCGCCAAAGAGTTGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3356  
QY 3484 TCAACACATTTGATGAG 3543  
Db 3357 TCAACACATTTGAG 3416  
QY 3544 GCGTGTCTTACTGAG 3603  
Db 3417 GCGTGTCTTACTGAG 3476  
QY 3604 GCGCCCTTGTATGATGAG 3663  
Db 3477 GCGCCCTTGTATGATGAG 3536  
QY 3664 TGGAGATGAG 3723  
Db 3537 TGGAGATGAG 3596

QY 3724 ACCTGCCCCCGGCTGCTACAAATACCAGGCTTTGAGCAACAGTGAAGCTGTAGAG 3783  
Db 3597 ACCTGCCCCCGGCTGCTACAAATACCAGGCTTTGAGCAACAGTGAAGCTGTAGAG 3656  
QY 3784 ATTCTCTCAAAAGTTCTGGATTCAGACTTACAGCTTGTAGAGATTCTCA 3837  
Db 3657 ATTCTCTCAAAAGTTCTGGATTCAGACTTACAGCTTGTAGAGATTCTCA 3710  
RESULT 8  
AAD31145  
ID AAD31145 standard; cDNA; 3582 BP.  
XX  
AC AAD31145;  
XX  
DT 21-AUG-2002 (first entry)  
XX  
DE Human laminin gamma2 chain cDNA.  
XX  
KW Cancer; cell proliferation; integrin receptor; signalling pathway;  
KW gene therapy; human; laminin gamma2; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..3582  
FT /tag= a  
FT /product= "laminin gamma2 chain"  
XX  
PN W0200230465-A2.  
PD 18-Apr-2002.  
PE 12-OCT-2001; 2001MO-US32127.  
XX  
PR 12-OCT-2000; 2000US-239705P.  
PR 24-OCT-2000; 2000US-242812P.  
XX  
PA (UNIP) UNIP ROCHESTER.  
XX  
PI Land H, Deleu L;  
XX  
DR WPI; 2002-416838/44.  
DR P-PSDB; AAE14712.  
XX  
PT Reducing proliferation of cancer cell, by inhibiting ligand binding to  
PT integrin receptor on cell, reducing integrin-integrin interaction,  
PT receptor clustering interaction or integrin-non-integrin protein  
PT interaction -  
XX  
PS Disclosure; Page 85-86; 148pp; English.  
XX  
CC The invention relates to a method of reducing proliferation of cancer  
CC cells, comprising inhibiting ligand binding to integrin receptor on  
CC cancer cells, where integrin receptor comprises integrin, reducing  
CC integrin-integrin interaction, integrin receptor clustering interaction  
CC or integrin-non-integrin protein interaction, reducing production of  
CC integrin or ligand of integrin receptor by cancer cells, or  
CC interfering with integrin-signalling pathway. The present sequence  
CC is human laminin gamma2 chain cDNA.  
XX  
SQ Sequence 3582 BP; 938 A; 872 C; 1026 G; 746 T; 0 other;  
Query Match 72.8%; Score 2904; DB 24; Length 3582;  
Best Local Similarity 89.1%; Pred. No. 0;  
Matches 3197; Conservative 0; Mismatches 370; Indels 21; Gaps 5;  
QY 198 ATGCTGCGCTGCTGAGAGCTGCTACTCTGCTCTGCTCTGCTGCGCGAGCCGG 257  
Db 1 ATGCTGCGCTGCTGAGAGCTGCTACTCTGCTCTGCTCTGCTCTGCTGCGCGAGCCGG 60  
QY 258 GCCACCTCCGGAGGAGAGAGTGTGTGATTCACAGGAGATTCAGGCAATGCAATCTTGAC 317





OY	2472	CAGGAGGCCACAGACATTTGGGACAGACGCCATGTTCTAGTCAGCCAGATACATGATGAGCACTG	2531
Db	2275	CAGGAGGCCACAAAGTTATGACAAAGGCCACGTTGATGATGACCCAGTAAATGATGAGCAACTG	2332
OY	2532	GCAAAAGAAACCACGAGTATTTCCAAAGAGCTGATGTACTGTGTGCGGAGGCTTCGAG	2591
Db	2335	ACAAAGGAAAACTGAGAGCTATTTCCAAACAGCCCTCTACGTGTGCGCAAGGCCCTGCAT	2394
OY	2592	GAAGAG-----GGGGAAGCGCGCGCCTGGAGCGGAGCGCGTGTGTGCAAAAGGCTGTGGGA	2645
Db	2395	GAGGAGTGTGGAAGCGGGAAGCGGTATGCCCGGACGGTGTGTGTGTCAAGGGCTGTGGAA	2455
OY	2646	AAATTGCAGAAAACCTAAATCTGTGGCCAGGAGTGTGAGGAGGCCACCGCAACCGAC	2705
Db	2455	AAATTGCAGAAAACCAAGCTCCCTGGCCAGAGTGTGACAAAGGAGGCCACTCAACCGGAA	2514
OY	2706	ATGGAAGAGATAGGTCCTTATCAGATATGTCTCCACCTTCATATCCGTGTCTCAGATT	2765
Db	2515	ATTGAAGAGATAGGTCCTTATCAGCAGTCTCCGCCCTCTCGGATTCAGTGTCTGCGCTT	2574
OY	2766	CAGGAGTCAATGATCAGTCTCCTTGCAGGT---AGAGGGAAGAGGCTCAGACAAAAACCT	2822
Db	2575	CAGGAGTCAAGTATCAGTCTCCTTCAGGTGGAAGAAGCAAGAGGATCAAAACAAAACCG	2632
OY	2823	GATTCTCTCTCAACCGTGTGACTATGACATATGATGATTCAGCACAGCTGCACAAACAT	2882
Db	2635	GATTCTCTCTCAACCGTGTGACTATGATGATTCAGCACAGCTGCACACAAAAGAT	2694
OY	2883	CTGGGAACCTGGGAGAGAAGAAACCCGGGAGCTCTACAGATGGGAAGAAATGGGGAGAG	2942
Db	2695	CTGGGAACCTGGGAAGAGAAGAACGACAGCAGACTCTTACGAATGGAAAAAGTGGGAGAG	2755
OY	2943	ACATCAGATCAGCTGCTTTCCCGTGCACAACTTGCTAAAGCAGAGCCCAAGAACCACTA	3002
Db	2755	AAATCAGATCAGCTGCTTTCCCGTGCACAACTTGCTAAAGCAGAGCCCAAGAACCACTG	2814
OY	3003	AGTATGGGCATGGCCACTTTTATGAAATGTAGAACATCTTAAGAAATCTCAGAGAGTTT	3062
Db	2815	AGTATGGGCATGGCCACTTTTATGAAATGTAGAACATCTTAAAAACCTCAGAGAGTTT	2874
OY	3063	GACCTGCAGGTTGGATTAAGAAAGACAGAAAGCTGAAAGGCCATGAAGAGACTCTCCATC	3122
Db	2875	GACCTGCAGGTTGGACAAACAGAAAGCAGAAAGCTGAAAGGCCATGAAGAGACTCTCCATC	2932
OY	3123	ATCAGACCAAGAGTTGGTGCAGGTGCCAGTCAACAAGACGAAGCAAGCAAGACCCCTGGGC	3182
Db	2935	ATCAGACCAAGAGTTTTCAGATGCCAGTACAAAGACCCAGCAAGCGAAGAAAGCCCTGGGC	2994
OY	3183	AGTGTGTGTCGCCAGCGCCACAGAGGGCAAGAATGACGACGAGGAGGCCCTGTGAGATCTCT	3242
Db	2995	AGCGTGTGCTGATGATGACACAGAGGCCAAGAAATGGGGCCGGGAGGCCCTGTGAAATCTCC	3055
OY	3243	GGCAAGATAGAAACAGAGATAGAGAGTCTGAACCTTGAAGCCAAATGTGACAGCAGATGGA	3302
Db	3055	AGTGAGATTGAACACAGAGATATGGGAGTCTGAACCTTGAAGCCAAATGTGACAGCAGATGGA	3114
OY	3303	GCCTTGGGCATGAGGAAGGAGACTGGCCACTGTGAAGAAATGAGATGAGAGAACTGTGAAGA	3362
Db	3115	GCCTTGGGCATGAGGAAGGAGACTGGCCCTCTCTGGAAGAAATGAGATGAGGGAAGTGTGAAGA	3174
OY	3363	GAGCTGTCAAGGAAGAGACAGAGAGTTTACATGATATGAGACGCGAGTCCAGATGGTAATT	3422
Db	3175	GAGCTGTCAAGGAAGAGAGACTGGAGTTTACACAGAAATATGATATGCAAGTACAGATGTGATT	3234
OY	3423	GCAGAGGCCCAAGAGATTGAAGAAACAGAGCCAAAGAAATGCTGAGATTACGATCCAAAGACA	3482
Db	3235	ACAGAGGCCCAAGAGATTGATACCAAGAGCCAAAGAACTGTGGGTTTACATCCAAAGACACA	3294
OY	3483	CTCAACACATTTGGATGGCATCTCTACCTATATAGCCCAAGCCCTGGCAGTGTGGATGAAGAG	3542
Db	3295	CTCAACACATTTAGACGGCTCTCGTATTTGATGACACAGCCCTCTCAGTGTGATGAAGAG	3354

	3543	3355	3603	3415	3663	3475	3723	3535
QY	AGCGTGAATCTTACATCGACACAAAGCTTTCCGAGCCAAAGCTCAGATCAACAGCAGCTA	GGCTTGGTCTTACTTACGTGACACAGACTTTCCCGAGCCAAAGCCAGATCAACAGCCAACTG	CGGGCCCTTGATGTCTAGAGCTGGAAAGAGAGGGGCACATCGGCAGAAAGGGCCACTCCGTTTC	CGGGCCCATGATGTCTAGAGCTGGAAAGAGAGGGGCACAGCTCAGCAGAGAGGGGCCACTCCGATTTG	CTGGAGACTACCATATGATGGGATTCCTGGCTGATGTGAAAGACCTTGGAGAACATCAAGGGAC	CTGGAGACAAACCATATGATGGGATTCCTGGCTGATGTGAAAGAACTTGGAGAAACATTTAGGGAC	AACTGACCCCGGGCTGCTACAATAACCCAGAGCTCTTGAGCAACAGTGA	AACCTGCCCCCAGGCTGCTACAATAACCCAGGCTCTTGAGCAACAGTGA
Db	3543	3355	3603	3415	3663	3475	3723	3535

RESULT 9  
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ID AAC83732 standard; cDNA; 3620 BP  
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AAC83732

DT 02-MAR-2001 (first entry)  
yy

DE Human laminin 5 CDNA, SEQ ID NO: 31

KW Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;

KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation; ss.

OS Homo sapiens

PN W0200066731-A2

PD 09-NOV-2000

PF 28-APR-2000; 2000WO-US11459.

PR 30-APR-1999; 99US-0131720.

PR 24-SEP-1999; 99US-0155945.

PA (BIOS-) BIOSTATUM INC

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DR WPI; 2000-687538/  
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PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery, burns, acute wounds and skin grafts

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CC laminin 5-expressing cells are used to accelerate wound healing,

CC surgery, burns, acute wounds, skin grafts, corneal ulcerations,

used to improve the biocompatibility of medical devices, and to promote

CC of Type I diabetes. Laminin can also be used to regulate angiogenesis. CC of Type I diabetes. Laminin can also be used to regulate angiogenesis.

CC whereas prior art cell lines have been created that produce but do not

XX

sequence 3620 BP; 959 A; 862 C; 1040 G; 759 T; 0 other;

Query Match	72.2%; Score 2880.8; DB 21; Length 3620
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Matches 3184; Conservative 0; Mismatches 387; Indels 21; Gaps 5;

OY	261	ACCTCCGGGAGGAAAGCTGTGATTTGCAACGGGAGTCCAGGCATTCATCTTTAGCACG	320
Db	1	ACCTCCAGAGGAGGAAGTGTGTGATTTGCAATGGGAAGTCCAGGCATGTATCTTTATCCG	60
OY	321	GAACCTTCACAAACAGACAGAAATGGATTCCGCTCCCTCACTCGAATGACAAACACTGAT	380
Db	61	GAACCTTCACAGAACACTGTGTATATGGATTCCGCTCCCTCACTCGAATGACAAACACTGAT	120
OY	381	GGCATCCACTGCGAGAGGTGCAAGGCGAGGATTTTACGACAGAGAGAAAGGAGCCGTGT	440
Db	121	GGCATCTCACTCGAAGAAATGCAAGAAATGGCTTTTACCGGACAGAGAAAGGAGCCGTGT	180
OY	441	TTACCCCTGCAATTTGTAACCTTAATAAGGTCTCTTACCCTCGAATGTGACAACTCTGGAGG	500
Db	181	TTGGCCCTGCAATTTGTAACCTTCACAAAGGTTCTCTTAAGTGTGATGTGACAAACTCTGGAGG	240
OY	501	TGCAGCTGTAAAGCCAGGTGTGACAGGAGACAGGTGTGACCCGATGTCTGCCCGCTTCCAC	560
Db	241	TGCAGCTGTAAACCAAGGTGTGACAGGAGCCAGATGCCAGATGTCTGCCAGGCTTCCAC	300
OY	561	ACACTCACTGATGCTGGGTGCGCCACAGACCAAGGCTGTAGACTCCAAAGTGTGACTGT	620
Db	301	ATGTCTCACTGATGTGGGGGTGCAACCCAAAGAACAGATGTGTAGACTCCAAAGTGTGACTGT	360
OY	621	GACCCAGCTGGCATCTCGAGGGCCCTGTGATCAGGCGCTGTGTGTGCAAGCCGCTGTGC	680
Db	361	GACCCAGCTGGCATCTCGAGGGCCCTGTATACGGGGCCGCTGTGTGTGCAAGCCACTGT	420
OY	681	ACTGGAGAGCCCTGTGTAGGTGTGTGACAGAGTGTACTATCACTGTGATGGGGAAACCT	740
Db	421	ACTGGAGAGCCCTGTGTATGGGTGTGTGATCAGGTTACTATATCTGTGATGGGGAAACCT	480
OY	741	CAGGGCTGTACCCAGTGTTTTGGCTATGTGGCATTTCCGACGTGCCACAGCTCTGGGGAC	800
Db	481	GAGGGCTGTACCCAGTGTTTTCTGTATGTGGCATTTACGACAGTGTCCGACAGCTCTCAGAA	540
OY	801	TACAGTGTCCATAAATATCATCTCTCCCTCATCAAGATGTGTATGGGTGGAAAGGCTGTGC	860
Db	541	TACAGTGTCCATAAGATATCACTCTTTCATTCAGAAATGTTGATGGCTGGAAAGGCTGTGC	600
OY	861	CAAGAAAGAGGGGTCTCTGTCAAAGCTCCAGTGTGTCACAGCGCCATCGGGAATATATTATAGC	920
Db	601	CAAGAAATATGGGTCTCTGTCAAAGCTCCAAATGTGTACAGCGCCATCAAGATGTGTTTATAGC	660
OY	921	TCAGCAGACAGCATCAGACCTGTGTATTTTGTAGTCTCTGCCAAATTTCTTGGGAATCAA	980
Db	661	TCAGCACCACAGCATAGACCTGTGTATTTTGTGGCTCTCTGCCAAATTTCTTGGGAATCAA	720
OY	981	CAGGTGAGACTACGGGCAAAAGCTATCTTTTGACTACACGCTGTGGATAGAGGGAGGACAGAC	1044
Db	721	CAGGTGAGACTATGGGCAAAAGCTGTCTTTTGACTACACGCTGTGTGACAGAGAGGACAGAC	780
OY	1041	CCATCTGCGCATGACGTGATCTCTGGAAAGTGTCTGTCTACGGATCACAAGCTCCCTTGATG	1100
Db	781	CCATCTGCGCATGTATGTATCTCTGGAAAGTGTCTGTCTACGGATCACAAGCTCCCTTGATG	840
OY	1101	CCACTGTGCAAGAACCTGCTGTGTGGGATACCAAGACTTTCACATTCAGATTAATATGA	1166
Db	841	CCACTGTGCAAGAACCTGCTGTGTGGGCTCACCAAGACTTTCACATTCAGGTTAAATGAG	900
OY	1161	CATCCAAAGCAATTTGGAGCCCCCAGCTAAGTACTTCTTGTGATATCGAGAGTCTTACTCGCG	1222
Db	901	CATCCAAAGCAATTAATTTGGAGCCCCCAGCTGAGTACTTCTTGTGATATCGAAGGTCTACTCGCG	960
OY	1221	AACCTCACAGCCCTGCGGATCCGAGCTACCTACGGAATATACGTAAGTCTGGTACATTGAC	1288
Db	961	AATCTTCACAGCCCTCCCGCATCCGAGCTACATATGGAGAAATACGTAAGTCTGGTACATTGAC	1020
OY	1281	AACGAGACCTTGATTTAGCCCGCCGCTTCTGTGAGCCCAAGGCGCCCGGGGTATGAACAA	1344
Db	1021	AATGTGACCTTGATTTAGCCCGCCCTGTCTGTGAGCCCAAGCACCCTGGGTTGTAACAG	1088

QY	1341	TGTGATGCGCTGTGGCTAACAGGGGAGATTCTCCAGGANTGTGGCTCCGGCTACAA	1400
Db	1081	TGTATATCTCTGTGGGTACAAAGGGCAATTCTCCAGGATGTGGCTTCGCTACAA	1140
QY	1401	AGAGATTCAGGACAGCTGGGACCTTTTGGACCTGTATTCATGTAACTGGCAAGGGGA	1460
Db	1141	AGAGATTCAGGAGAGCTGGGCTTTTGGACCTGTATTCCTTGTAACTGCCAAGGGGA	1200
QY	1461	GGGGCTTCGATTCAGACACAGAGAGACTGTTACTACAGGGATGTGAACCTCGACATCCT	1520
Db	1201	GGGGCTTCGATTCAGACACAGAGAGATGTATTACAGGGATGTGAATCCTGCATAT	1257
QY	1521	GAGTGTGCTGACTGCCCATTTGTTCTACACGATCCACAGACCCCGCAGCTGCAG	1580
Db	1258	GAGTGTGCTGACTGCCCAATTGGTTTCTACAAACATCCGCACGACCCCGCAGCTGCAG	1317
QY	1581	CCGTGCCCCCTTCGGAATGGGTTCAGCTGCTCCGTGATTCCTGTAGACAGAGAGTGGTG	1640
Db	1318	CCATTCCTCTGTCATACGGGTTACGCTGCTACGATGATGCCGAGAGCGAGAGTGGTG	1377
QY	1641	TGCATATACTCCCCCAGGAGTGTCACTGTCACCGCTGTGAGCTCTGTGATAGGCTAT	1700
Db	1378	TGCATATACTGCCCTCCCGGGGTACACGGTCCCGCTGTGAGCTCTGTGATAGGCTAC	1437
QY	1701	TTTGGGGACCCCTTGGGGAACTGTCGCCAGTGAAGGCTTGTCAAGCCTGTCACTGCAC	1760
Db	1438	TTTGGGGACCCCTTGTGGTGAACATGCGCCAGTGAAGGCTTGTCAAGCCTGTCAATGCAC	1497
QY	1761	AACACGTGGACCCCTGATCCCTCCGGGAACGTACACCGCTGCAGACGAGGTGTGTGAG	1820
Db	1498	AACACGTGGACCCCAAGTCCCTCTGGGAATGTGACCCGGTGACAGGAGGTGTGTGAG	1557
QY	1821	TGCATACACACACAGCTGGGGGTCCACATGTACACAGTCCAAAGCAGCTACTATAGGGAC	1880
Db	1558	TGTATCCACACACAGCCGGGCACTACTGCGACACAGTCCAAAGCAGCTACTTGGGGAC	1617
QY	1881	CGTTGGCTCCCATTCACGACAGCAAGTGTGAGCTTGCACATGCACCCACAGTGGCTCG	1940
Db	1618	CCATTTGGCTCCCAACCCAGCAGACAAAGTGTGAGCTTCACTGTAAACCCATGGGCTCA	1677
QY	1941	GAGCCTGTGAGAGTGTCCGAAGTATGGGACGCTGTGTTCCAAAGCAGCTTGTGTGGCTC	2000
Db	1678	GAGCCTGTGAGAGTGTCCGAAGTATGGGACGCTGTGTTCCAAAGCAGGATTTGTGGCCCC	1737
QY	2001	AGCTGTGAGCAGTGGGCACTGACACGAGCTGTCCAGCTTCTCTTAATCAAGTAAGTTAG	2060
Db	1738	AACGTGTGAGCAGTGGGCACTT---CAGCTGTCCAGCTTCTCTTAATCAAGTAAGTTAG	1794
QY	2061	ATGATCATGTTATGACAGCAGCTCCAGATCCTGAGAGCCCTGATTTCCAAAGGCTCAGG	2119
Db	1795	ATGATCATGTTATGACAGCAGCTCCAGAGATGGAAGTGGAGCCCTGATTTCAAAGGCTCAGG	1854
QY	2120	-----TGAGCAGTATCCCAAGCAGAGCTGGAAAGGACAGATGACAGAGCTGACAGGCC	2174
Db	1855	GGTGATGAGAGTATCCTGATACAGAGCTGGAAAGGACAGATGACAGAGCTGACAGGCC	1914
QY	2175	CTTCGGGACATTTCTAGAGAAAGCCAGATTTCCAAAGATGCTGTTAGATCCTTCAATCTC	2234
Db	1915	CTTCGGGACATTTCTAGAGATGCCCCAGATTTCCAAAGTGCCTAGCAGATCCTTGTGTCTC	1974
QY	2235	CGGGTGGCCAAAGGACGCTCAAGAGATAGCTACCGGAGCCGCTGGATGACCTCAAG	2294
Db	1975	CAGTTGGCCAAAGGTGAGGAGCCAAAGAAAGACAGTCTCCAGACCCGCTGGATGACCTCAAG	2034
QY	2295	ATGATCTGTGGAAGAGTTCCGGGCCCTGGGCACTCAGTATTCGAAMCCAGTTCCAGATATCT	2354
Db	2035	ATGATCTGTGGAAGAGTTCCGGGCCCTTGGGAAGTCAAGTCCAGAACCCGATTCGGGATATCT	2094
QY	2355	CGCAGGCTCATACACTCAGATGCGGCTTGAGCCTGGAGGAAGTGAAGGCTTCCCTGCAAAAC	2414
Db	2095	CACAGGCTCATACACTCAGATGAGCTGAGCCTGGCAGAAATGAAGCTTCTTGGGAAC	2154
QY	2415	ACCAACATCTCTCTTCAGAGCACTACCTGTGGGCCCAATGCTTTAAAGTCTGGCTCAG	2474

Db 2155 ACTACATCTCTGCTGAGACCACTACGTGGGGCAATGGCTTTAAACCTGGCTCAG 2214  
 QY 2475 GAGGCCACGAGATTGGGACAGACCATGTTCACTACAGCCAGTAACATGAGCACTGGCA 2534  
 Db 2215 GAGGCCACGAGATTGAGCAAGACCATGTTGAGTCAAGCCAGTAACATGAGCACTGGCA 2274  
 QY 2535 AAGGAACCCAGAGATGTTCCAAAGAGCTGATGCTAGTGGCGGAGGCTCTGACGAA 2594  
 Db 2275 AGGGAACCTGAGGCTATCTCAAAACAGCCCTCACTGCTGGCGCAAGCCCTGCATGAA 2334  
 QY 2595 GGAG-----GCGGAACCGGACGCTTGAGAGGAGCCCTGGTGCAGAGGCTTGGGAAA 2648  
 Db 2335 GAGGTGCGAAGCGGAGACGGGTAGCCGCGAGGTGGTGGTGCAGAGGCTTGGGAAA 2394  
 QY 2649 TTGCGAAGAACTAAATCTCTGCGCCAGAGAGTGTGCGAGGAGGCGCAACCGACATC 2708  
 Db 2395 TTGCGAAGAAACCAAGTCCCTGCGCCAGCACTTGCAGAGGAGGCGCACTCAAGCGGAAT 2454  
 QY 2709 GAAGCAGATAGTCTTATCAGCATAGTCTCCACCTTCTCAATTCCTGCTCAGATTGAG 2768  
 Db 2455 GAAGCAGATAGTCTTATCAGCATAGTCTCCACCTTCTCAATTCCTGCTCAGATTGAG 2514  
 QY 2769 GAGTCAATGATAGTCTTGCAGGT---AGAACCGAAGGCTCAGACAAAAGCTGAT 2825  
 Db 2515 GAGTCAATGATAGTCTTGCAGGT---AGAACCGAAGGCTCAGACAAAAGCTGAT 2574  
 QY 2826 TCTCTCAAAACCGTGTGACTTAAGCATATGATGATGATGATGATGATGATGATGATGAT 2885  
 Db 2575 TCACTCTCAAGCTCGTATACACAGCATATGATGATGATGATGATGATGATGATGATGAT 2634  
 QY 2886 GGAACCTGGAGAGAGAAACCCGCGAGCTCTTACAGATGAGAAAGAAAGAGAGACAGACA 2945  
 Db 2635 GGAACCTGGAGAGAGAAACCCGCGAGCTCTTACAGATGAGAAAGAAAGAGAGAGAA 2694  
 QY 2946 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3005  
 Db 2695 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2754  
 QY 3006 ATGGGCATGCCACTTTTATGAGATGAGAACTCTTAAAGATCAGAGAGTTTGGAC 3065  
 Db 2755 ATGGGCATGCCACTTTTATGAGATGAGAACTCTTAAAGATCAGAGAGTTTGGAC 2814  
 QY 3066 CTCAGAGTTGAGATTAAGAGCAAGAGCTGAAAGGCGCATGAGAGACTCTCTACATC 3125  
 Db 2815 CTCAGAGTTGAGATTAAGAGCAAGAGCTGAAAGGCGCATGAGAGACTCTCTACATC 2874  
 QY 3126 AGCCAGAGTTGAGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 3185  
 Db 2875 AGCCAGAGTTGAGATGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 2934  
 QY 3186 GCTGCTGCCAGCCGAGAGGCAAGAAATGACAGAGGAGGCGCTGAGATCTCGGC 3245  
 Db 2935 GCTGCTGCCAGCCGAGAGGCAAGAAATGAGGCGCGGAGGCGCTGAGATCTCGGC 2994  
 QY 3246 AACATGAGAGAGATGAGAGGTCTGAACTTGGAAACCAATGATGACAGAGATGAGCC 3305  
 Db 2995 GAAATGAGAGAGATGAGAGGTCTGAACTTGGAAACCAATGATGACAGAGATGAGCC 3054  
 QY 3306 TTGGCATGGAGAGAGGAGTGGCCACTCTGAAAGAGATGAGAGAGAGAGAGAGAG 3365  
 Db 3055 TTGGCATGGAGAGAGGAGTGGCCACTCTGAAAGAGATGAGAGAGAGAGAGAGAGAG 3114  
 QY 3366 CTGTCAAGAGAGAGAGAGGATTTGACATGATGAGAGCCAGTGCAGATGATGATGATGAT 3425  
 Db 3115 CTGTCAAGAGAGAGAGGATTTGACATGATGAGAGCCAGTGCAGATGATGATGATGATGAT 3174  
 QY 3426 GAGGCCCAAGAGATGAG 3485  
 Db 3175 GAGGCCCAAGAGATGAG 3234  
 QY 3486 AACACATTTGATGAGATCTTACACCTTAATGAGACAGGCTGGAGTGGATGAGAGAGAG 3545

Db 3235 AACACATTTAGACGAGCTCTCTGATCTGATGAGAGACGCTCTCTGATGATGAGAGAGAG 3294  
 QY 3546 CTGATCTTACTGAG 3605  
 Db 3295 CTGATCTTACTGAG 3354  
 QY 3606 CCTTGTGTCAGAGCTGGAAG 3665  
 Db 3355 CCTTGTGTCAGAGCTGGAAG 3414  
 QY 3666 GAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3725  
 Db 3415 GAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3474  
 QY 3726 CTGCCCCCGGCTGCTCAATTAACAGAGCTCTTGAAGCAAGAGAGAGAGAGAGAGAGAG 3785  
 Db 3475 CTGCCCCCGGCTGCTCAATTAACAGAGCTCTTGAAGCAAGAGAGAGAGAGAGAGAGAG 3534  
 QY 3786 TTCTCAACCAAGGTTCTTGGGATTCAGACCTAGCTGCTTGAAGATTTCTCA 3837  
 Db 3535 TTCTCAACCAAGGTTCTTGGGATTCAGATCTCAGGCTCGGAGAGCATGTCA 3586  
  
 RESULT 10  
 AAC83730  
 ID AAC83730 standard; cDNA; 5020 BP.  
 XX  
 AC AAC83730;  
 XX  
 DT 02-MAR-2001 (first entry)  
 XX  
 DE Human laminin 5 cDNA, SEQ ID NO: 27.  
 XX  
 KW Human; laminin 5; vulnerary; antiulcer; antiinflammatory; antidiabetic;  
 KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;  
 KW periodontitis; gingivitis; type I diabetes; angiogenesis regulation; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200066731-A2.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PE 28-APR-2000; 2000WO-US11459.  
 XX  
 PR 30-APR-1999; 99US-0131720.  
 PR 21-AUG-1999; 99US-0149738.  
 PR 24-SEP-1999; 99US-0155945.  
 XX  
 PA (BIOS-) BIOSSTATUM INC.  
 XX  
 PI Boutaud A;  
 XX  
 DR WPI: 2000-687538/67.  
 DR P-PDB; AAB48469.  
 XX  
 PT Laminin 5-expressing cells, used to accelerate wound healing associated  
 PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,  
 PT burns, acute wounds and skin grafts -  
 XX  
 PS Claim 4; Page 185-191; 232pp; English.  
 XX  
 The present sequence encodes a laminin 5 chain polypeptide. Recombinant  
 CC laminin 5-expressing cells are used to accelerate wound healing,  
 CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin  
 CC surgery, burns, acute wounds, skin grafts, corneal ulcerations,  
 CC gastro-intestinal ulcers, periodontitis, and gingivitis. They are also  
 CC used to improve the biocompatibility of medical devices, and to promote  
 CC cell adhesion to a surface. They can be used for the ex vivo treatment  
 CC of Type I diabetes. Laminin can also be used to regulate angiogenesis.  
 CC The cell line produces and secretes recombinant heterotrimeric laminin,  
 CC whereas prior art cell lines have been created that produce but do not  
 CC secrete only one or two chain laminins.

XX Sequence 5020 BP; 1329 A; 1170 C; 1333 G; 1188 T; 0 other;  
SQ  
Query Match 72.2%; Score 2879.2; DB 21; Length 5020;  
Best Local Similarity 88.6%; Pred. No. 0;  
Matches 3183; Conservative 0; Mismatches 388; Indels 21; Gaps 5;

QY 261 ACCTCCGGAGGAGAGTCTGTGATGACAGCGGAGAGTCCAGGCAATGCATCTTTGACCAG 320  
DB 1 ACCTCCAGAGAGGAGAGTCTGTGATGCAATGGAGAGTCCAGGCAATGCATCTTTGAGCCG 60  
QY 321 GAATTTACAAACAGACAGAAATGATTCCTGCTGCTCAATGCAATGACACACTGAT 380  
DB 61 GAATTTACAAACAGACAACTGTAAATGATTCCTGCTGCTCAATGCAATGACAACTGAT 120  
QY 381 GGCATTCACAGCGAGAGTGCAGAGCAAGATTTACGACAGAGAGAAAGGAGCCGCTGT 440  
DB 121 GGCATTCACAGCGAGAGTGCAGAGCAAGATTTACGAGGACAGAGAAAGGAGCCGCTGT 180  
QY 441 TTACCTGCAATTTGTAATCTTAAGGTTCCTTAAGCCTCGATGTCACAACTCTGACGG 500  
DB 181 TTGCGCTGCAATTTGTAATCTTAAGGTTCCTTAAGTGTGATGTCACAACTCTGACGG 240  
QY 501 TGCAGCTGTAAAGCCAGGTGTGACAGAGACAGGTGTACGATGTCTGCCGCTTCAC 560  
DB 241 TGCAGCTGTAAAGCCAGGTGTGACAGAGCCAGATGTCTGCCAGGCTTCAC 300  
QY 561 ACACTACTGATGTGGGGTGGCCAGACCAAGAGGCGTGAAGTCCAAAGTGTGACTGT 620  
DB 301 ATGCTCACGATGTGGGGTGGCCAGACCAAGAGACTGTGACTCCAAAGTGTGACTGT 360  
QY 621 GACCCAGCTGGCATCTAGGGCCCTGTGACTAGGCGCGTGTCTGTGCAAGCCGCTGTC 680  
DB 361 GACCCAGCTGGCATCTAGGGCCCTGTGAGCCGCGCTGTGTCTGCAAGCCGCTGTC 420  
QY 681 ACTGAGAGCGCTGTGATAGTGTGACAGAGGTTACTATCACTCTGATGGGGAACCTT 740  
DB 421 ACTGAGAGCGCTGTGATAGTGTGACAGAGTACTATCACTCTGATGGGGAACCTT 480  
QY 741 CAGGGCTGTACCAAGTGTGTTTGTGATGGGCAATCCGACAGTGCACAGTCTGGGGAG 800  
DB 481 GAGGGCTGTACCAAGTGTGTTTGTGATGGGCAATCCGACAGTGCACAGTCTGGGGAG 540  
QY 801 TACAGTGTCCATAAATCATCTCTGCTTCATCAAGATGTGTGATGGCTGGAAGGCTGTC 860  
DB 541 TACAGTGTCCATAAATCATCTCTGCTTCATCAAGATGTGTGATGGCTGGAAGGCTGTC 600  
QY 861 CAAAGAAAGCGGTCTCTGCAAAAGTCCAGTGTGACAGGCGCATCGGATATATTATG 920  
DB 601 CAAAGAAATGGGTCTCTGCAAAAGTCCAAATGTCACAGCGCATCAAGATGTGTTAGC 660  
QY 921 TCAGCAGAGCATCAGACCTCTGTCTATTTTGTAGCTCTGCCAAATTTCTTGGGAAATCA 980  
DB 661 TCAGCAGCAGCATCAGATCTCTGTCTATTTTGTGCTCTCTGCCAAATTTCTTGGGAAATCA 720  
QY 981 CAGGTGAGCTACGGGCAAAAGCCTATCTTTGACTACCTGTGTGATGGGAGGCGACAGAC 1040  
DB 721 CAGGTGAGCTATGGGCAAAAGCCTGTCTTGTACTACCTGTGTGAGAGAGGAGCGACAGAC 780  
QY 1041 CCATCTGCCCATGTGATCTCTGTGAGAGTGTCTGCTACGAGATACAGCTCCCTTGTATG 1100  
DB 781 CCATCTGCCCATGTGATCTCTGTGAGAGTGTCTGCTACGAGATACAGCTCCCTTGTATG 840  
QY 1101 CCACCTTACAGACAGCTGCTGTGGGATTCACCAAGACTTACACTTACAGATTAATAATA 1160  
DB 841 CCACCTTACAGACAGCTGCTGTGGGATTCACCAAGACTTACACTTACAGATTAATAATAG 900  
QY 1161 CATCCAAAGCAGTAATTGGAGCCCGAGCTAAGTTACTTGAATCGAGAGTTACTGCGG 1220  
DB 901 CATCCAAAGCAGTAATTGGAGCCCGAGCTAAGTTACTTGAATCGAGAGTTACTGCGG 960  
QY 1221 AACCTCACAGCCCTGCGGATCCGAGCTACCTACGAGAGATACAGTACTGGGTACATTTGAC 1280  
DB 1221 AACCTCACAGCCCTGCGGATCCGAGCTACCTACGAGAGATACAGTACTGGGTACATTTGAC 1280

DB 961 AATCTCACAGCCCTCCGCAATCCGAGCTACATATGAGAAATACAGTACTGGGTACATTTGAC 1020  
QY 1281 AACGTACCTTGATTTGAGCCCGCCGCTTCTGTGAGCCCGCCGCTGGTGTGAACAA 1340  
DB 1021 AATGTACCCCTGATTTTACAGCCCGCCGCTCTCTGTGAGCCCGCCGCTGGTGTGAACAG 1080  
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DB 1081 TGTATATGCTCTGTTGGGTACAAAGGGCAATTTGCAAGATTTGCTTCTGCTGCTACAAAG 1140  
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DB 1141 AGAATTCAGGCAACAGCTGGGACCTTTTGGACCTGTATTCATATGTAATCTGCAAGGGGGA 1200  
QY 1461 GGGGCTGCGCATTCAGACACAGAGAGACTGTACTACAGGGAGTGAAGAACCCGACATCCCT 1520  
DB 1201 GGGGCTGTGATTCAGACACAGAGAGATTTGTTATTCAGGGAGTGAAGAACCTCTGACAT---T 1257  
QY 1521 GAGTGTGCTGACTGCCCCCATTTGTTTCTACAAAGATCCCAAGACCCCGCAGCTGCAAG 1580  
DB 1258 GAGTGTGCTGACTGCCCCCATTTGTTTCTACAAAGATCCGACAGACCCCGCAGCTGCAAG 1317  
QY 1581 CCGTGGCCCTGTCCGCAATGGGTGTGAGCTGCTCCGTGATAGCTGTGAGACAGAGAGAGTGTG 1640  
DB 1318 CCATGTCCCTGTGCAATTAAGGGGTTCAGCTGCTCACTGATTTCCGAGAGGAGAGAGTGTG 1377  
QY 1641 TGCATTAATCTGCCCCCAGAGGTGTCACTGTGCTCCGCTGTGAGCTGTGCTGATGGCTAT 1700  
DB 1378 TGCATTAATCTGCCCCCAGAGGTGTCACTGTGCTCCGCTGTGAGCTGTGCTGATGGCTAT 1437  
QY 1701 TTTGGGGACCCCTTTCGGGGAAAGTGGCCCAAGTGAAGGCTTGTGACCCCTGTCAAGTGCAC 1760  
DB 1438 TTTGGGGACCCCTTTCGGGGAAAGTGGCCCAAGTGAAGGCTTGTGACCCCTGTCAATGCAAC 1497  
QY 1761 AACCAAGCTGACCTAGTGCCTCCGGGACAGTGTACAGCCCTGACAGAGAGAGTGTGTAAG 1820  
DB 1498 AGCATGTGGAAGCCCAAGTGTCTGGGAATTTGACCGGCTGACAGAGAGAGTGTGTAAG 1557  
QY 1821 TGCATTCACACACAGCTGGGGTCCACTGTACAGCAAGTGCACAGAGCTTACTATATGGGAG 1880  
DB 1558 TGTATTCACACACAGCGCGGATGTACGTGACAGCAAGTGCACAGAGCTTACTATATGGGAG 1617  
QY 1881 CCGTGGCTCCCAATCCAGACAGCAAGTGTGAGCTTGCACACTGCAACCCAGTGGGCTG 1940  
DB 1618 CCATTTGGCTCCCAACCCAGACAGCAAGTGTGAGCTTGCACACTGCAACCCAGTGGGCTGCA 1677  
QY 1941 GAGCCTGTGAGTGTGCAAGAGTGTGAGCGTGTGTTCCAAAGCCAGGCTTGGTGGGCTC 2000  
DB 1678 GAGCCTGTGAGTGTGCAAGAGTGTGAGCGTGTGTTCCAAAGCCAGGATTTGGTGGGCTC 1737  
QY 2001 AGCTGTGAGCAATGGCGCACTGACAGCTGTCTCAGCTGTCTATTAATCAAGTGAAGTTGAG 2060  
DB 1738 AACTGTGAGCAATGGAGCAAT---CAGCTGTCCAGCTTCTATTAATCAAGTGAAGTTGAG 1794  
QY 2061 ATGATCAGTTTATGACAGCTCCAGATCTCGAGTCTGAGAGCCCTGATTTGGAAGCTCAGG- 2119  
DB 1795 ATGATCAGTTTATGACAGCTCCAGATCTCAGAGATGTGAGGCGCTGATTTCAAAGCTCAGGCT 1854  
QY 2120 -----TGAAGAGTACCCCAAGCAGAGCTGTGAAGGCAAGATGACAGAGCTGAGAGGCC 2174  
DB 1855 GGTGATGAGAGTATACCTGATACAGAGCTGTGAAGGCAAGATGACAGAGCTGAGAGGCC 1914  
QY 2175 CTGCGGACATTTCTGAGAGAGCCAGATTTCAAAAGTGTGTAGATCTCTCAATGTC 2234  
DB 1915 CTTCAGGACATTTCTGAGAGATGCCCCAGATTTTCAGAGAGTGTCTAGAGATCTCTTGTGTCTC 1974  
QY 2235 CGGCTGGCCAAAGGACATCAAGAGATAGCTACCGGAGCCGCTGGATGACCTCAAG 2294  
DB 1975 CAGTTGGCCAAAGGTGAGAGCAAGAGATAGCTACAGAGCGCGCTGGATGACCTCAAG 2034  
QY 2295 ATGACTGTGAAAGAGTTCGGGCTCTGGGCAAGTCAAGTATCAGAACCAAGTTCAAGATACT 2354  
DB 2035 ATGACTGTGAAAGAGTTCGGGCTCTGGGAGTCAAGTATCAGAACCAAGTTCAAGATACT 2094

QY	2355	CGCAGGCTCATCTACTCAGATGGGCGCTTGAGCCCTGGGAGGAAAGAGAGGCTTCCCTCGCAAAAC	2414
Db	2095	CACAGGCTCATCTACTCAGATGCTGAGGCTTGGCAGAAAGTGAAGCTTCTTGGGAAAC	2154
QY	2415	ACCAACATTTCTCTTTCAGAGCACTACGTGGGGCCAAATGGCTTTAAAGTCTGGCTCAG	2474
Db	2155	ACTAACATTTCTCTCTCGCTCAGACCACCTACGTGGGGCCAAATGGCTTTAAAGTCTGGCTCAG	2214
QY	2475	GAGGCGCAGAGATTGGCAGACAGCCATGTTCAAGTCCAGCCAGTAAACATGGACCAACTGGCA	2534
Db	2215	GAGGCGCAGAGATTGACAGAAAGCCACGTTAGTCAAGCAGTAACATGGACCAACTGGCA	2274
QY	2535	AAGGAAACCCAGGAGTATTTCCAAAGAGCTGATGTCATCTACTGTCGGCGAGGCTCTCGCAGAA	2594
Db	2275	AGGGAACATGAGGACTATTTCCAAACAAACCCCTCTACTGCTGTGGCGAAGGCCCTCGATGAA	2334
QY	2555	GGAG-----GCGGAGCGGCACGCTGAGCGAGCGAGCCGTGTGTGCAAAAGGCTTGTGGGAAA	2648
Db	2335	GGAGCTGGAGAGCGGAGGCGGTAGACCCCGGACGGTGTGTGTGCAAAAGGCTTGTGGAAAA	2394
QY	2649	TTGCGAAAAACCTAATCTCTGGCCCCAGAGTGTGTGAGGGAGGCCAGCCAAACCGACATG	2708
Db	2395	TTGGAGAAAAACCAATCCTCTGGCCCCAGAGTGTGTGACAAAGGAGGCGCACTCAAGCGGAAAT	2454
QY	2709	GAAGCAGATTAGGCTTTATCAGCATAGTCCACCTTTCATTTCCGTTCTCAGATTTCAG	2768
Db	2455	GAAGCAGATTAGGCTTTATCAGACAGCTCCGCCCTCTGGATTGATGTCTCCGGTTTCAG	2514
QY	2769	GGAGTCATAGTATCACTCCTTGCAGGT---AACAAGGAAGAGGCTCAGCAAAAAGCTGAT	2825
Db	2515	GGAGTCATAGTATCACTCCTTTCAGTGGAGAAAGAAAGAGAGATCAAAACAAAAGCGGAT	2574
QY	2826	TCTCTCTCAAAACCGTGTACTAAGCATATGGATGAGTTCAAGCAAGCTGCAAGCAATCTG	2885
Db	2575	TCACTCTCAAGCGCTGTAAACCAAGCATATGGATGAGTTCAAGCGTACACAAAAGATCTG	2634
QY	2886	GGAATCTGGGAAAGAAACCCCGGACGCTTTACAGAAATGGAAGAATGGAGACAGACA	2945
Db	2635	GGAATCTGGAAAGAAAGAAAGACAGACAGCTCTTACGAATGGAAAAAGTGGGAGAGAGAA	2694
QY	2946	TCAGATCAGCTGCTTCCCGTGCACAACTTCTTAAACCAAGCCCAAGAGCACTAGT	3005
Db	2695	TCAGATCAGCTGCTTCCCGTGCACATCTTCTCTAAAGCAAGCAAGAGCACTAGT	2754
QY	3006	ATGGGCAATGCCACTTTTATGAAATTGAGAAACATCTTAAAGAAATCTCAGAGATTGCAC	3065
Db	2755	ATGGGCAATGCCACTTTTATGAAATTGAGAGCACTCTTAAAAACCTCAGAGATTGCAC	2814
QY	3066	CTGCGAGTTGGAGATTAAGAGACGAACCTAACAAGCCATGAAGAGACTCTCTACATC	3125
Db	2815	CTGCGAGTTGGACAAACAGAAAGACGAACCTAAGAAGCCATGAAGAGACTCTCTACATC	2874
QY	3126	AGCCGAAAGATTGCGAGGTGCCAGTGACAAAGACGAAGCAAGCAGAAAGCAGCCCTGGGAGT	3185
Db	2875	AGCCGAAAGATTGTCAGATGCCAGTGACAAAGACCAAGCAGAAAGAGCCCTGGGAGAC	2934
QY	3186	GCTGCTGCCGACGCCACAGAGGGCAAAAGATCAGCCAGGAGAGCCCTGAGATCTTGCC	3245
Db	2935	GCTGCTGCTGATGACACAGAGGGCAAAAGATGGGGCCGGGAGGCCCTGGAAATCTCCAGT	2994
QY	3246	AAGATTAGAAACAGAGATATGAGAGTCTGAACCTTGGAAAGCCATGTGACAGCGAGATGGAGCC	3305
Db	2995	GAGATTGAACAGAGATTTGGAGTCTGAACCTTGGAAAGCCATGTGACAGCGAGATGGAGCC	3054
QY	3306	TTGGCCATGAGAAAGGCACTGGCCACTCTGAAAAGTGAATGAGAGAAAGTGTGAAGGAGAG	3365
Db	3055	TTGGCCATGAGAAAAGGCACTGGCCCTCTCTGAAAGTGAATGAGAGAAAGTGAAGGAGAG	3114
QY	3366	CTGTCCAGGAAGGAGCAAGGATTTTGACATGATATGACACGATGCGAGATGGTAAATTGCA	3425
Db	3115	CTGTGAAGGAAGGAGCTGGAATTTTGACACGAATATGATGTGACATGATGCTAATTAACA	3174

OY	3426	GAGGCCCCAAAGATTGGAAACAGAGCCCAAGAAATGCTGGAGTTTACATCAAGACACACTC	3485
Db	3175	GAGGCCCAAGAGGTTTGATACCAAGACCAGAACGCTGGGGTTTACATTCAGACACACTC	3234
OY	3486	AACACATTGGATGGCATCCTACACCTAATATAGACACAGCCTGGCAGTGTGGATGAAGAGAGG	3545
Db	3225	AACACATTAGACGGCCTCTCCATCTGATGTAGACACAGCCTCTCAGTGTGATGAAGAGGGG	3294
OY	3546	CTGATCTTACTGGAGACAGAACCTTTTCCGAGCCAAAGACTCAGATCCAAAGCCAGCTACGG	3605
Db	3295	CTGCTCTTACTGGAGACAGAACCTTTCCCGAGCCAAAGACCCAGATCCAAAGCCAACTGGG	3354
OY	3606	CCCTTGATGTAGAGCGTCGGAAGAGAGAGGGGCACATGGCGGAAGGGGCACCTCGTTTCCCTG	3665
Db	3355	CCCATGATGTAGAGCTCTGGAGAGAGGGGCACCTGACAGAGGGGGCACCTTCATTTCGTG	3414
OY	3666	GAGACTAGCATAGATGGGATTCCTGGCTGATGTGAAGAACCTTGAGAAATCATCAGGAGACAAAC	3725
Db	3415	GAGACAAGCATAGATGGGATTCCTGGCTGATGTGAAGAACTTGAGAAATCATTAGGGAGCAAC	3474
OY	3726	CTGCCCCCCGGGCTGCTACATATCCAGGCTCTTGAGCAACAGTGAAGCTGCTTTAGAGAT	3785
Db	3475	CTGCCCCCCAGGCTCTCAATATACCAGGCTCTTGAGCAACAGTGAAGCTGCTCAATAATAT	3534
OY	3786	TTTTCACAACGAAGTTCTTGGGATTCAGACCTAGCTAGCGCTTGAAGATTTTCTCA	3837
Db	3535	TTTTCACAATGAGTTCTTGGGATTCAGATTCACAGGCTCGGGAGCCATGTCA	3586

RESULT 11  
A0013334

ID AAT13324 standard; cDNA; 4316 BP.

AC AAT13324;

DT 13-NOV-1996 (first entry)

DE Kalinin/laminin 5 gamma-2 chain alternative coding sequence.

XX  
XX  
kaljintn: lamintn: endermolvasi bullosa: functional: probe:

KW detection; inhibit; monitor; malignancy; ss.

OS Homo sapiens

....	Key	Location/Qualifiers
------	-----	---------------------

FT	118.3433
FT	/*tau=
FT	h
CDS	

FT /note= "kalinin/laminin 5 gamma-2 chain"  
vv

PN W09610646-A1

PD 11-APR-1996.

XX 04-OCT-1995. 95W0-EP03918  
DE

XX	0470 0317450
XX	0470 0317450

XX

XX (1967) NOVEMBER

Pl Kallunki P, Pyke C, Tryggvason K;  
XX

DR WPI; 1996-209366/21.

XX

PT detect, monitor and inhibit the invasive growth of cell in tissue

partic. malignant tissue

PS Disclosure; Fig 4B; 37pp; English

CC The present sequence is cDNA (Genbank Z15009), with an alternativ

chain (R91428). The gamma-2 chain is of importance to patients suffering

CC from epidermolysis bullosa, esp. the junctional form (JEB). Probes and  
CC antisense gamma-2 sequences derived from this sequence can be used to  
CC detect, monitor and inhibit the invasive growth of cells in tissue,  
CC partic. malignant tissue.

XX Sequence 4316 BP; 1158 A; 1033 C; 1226 G; 899 T; 0 other;

Query Match 68.3%; Score 2726; DB 17; Length 4316;  
Best Local Similarity 88.5%; Pred. No. 0;  
Matches 3045; Conservative 0; Mismatches 365; Indels 30; Gaps 7;

QY 99 AAGGAAAAAGAGGACAGCGGAGCGGAGAGTGAATCCCAAGCGGCGAGCGCGGCG 158  
Db 14 AAGGAAAAAGAGGACAGCGGAGCGGAGAGTGAATCCCAAGCGGCGCGGCG 71  
QY 159 AGGACCCCTGACAGCGCG-----GACGGCGCGCGGCGCTGGCCATGGCTGGCGCTG 211  
Db 72 AGGACCCCTGACAGCGGAGAGAGAGTGAAGCGGCGCGGAGCGCGGCGCGCTG 131  
QY 212 GCTGAGCTGCTACCTCTGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 271  
Db 132 GCTGAGCTGCTGCTCTGCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 191  
QY 272 GGAAGTGTGATTGCAACGAGGAAAGTCCAGGCAATGCATCTTTGACAGAACTTCA 331  
Db 192 GGAAGTGTGATTGCAATGGGAAGTCCAGGCAATGCATCTTTGATGCGGAACTTCA 251  
QY 332 ACAGACAGGAAATGGATTCGGCTGCTCAACTGCAATGACAAAGCACTGATGCCATG 391  
Db 252 ACAAGCTGTAAAGATTCGGCTGCTCAACTGCAATGACAAAGCACTGATGCCATG 311  
QY 392 CGAGAGGTGCAAGGACGAGATTTTACCGACAGAGAAAGGAGCGCTGTTTACCTCCAA 451  
Db 312 CGAGAGGTGCAAGAAATGGCTTTTACCGGACAGAGAAAGGAGCGCTGTTTACCTCCAA 371  
QY 452 TTGTAATCTTAAAGGTTCTCTTAAAGCTCGATGTGACAACTCTGACGCTGACCTG 511  
Db 372 TTGTAATCTTAAAGGTTCTCTTAAAGCTCGATGTGACAAAGCTGACGCTGACCTG 431  
QY 512 GCCAGGTGTGACAGAGAGAGAGGTGTACCGGATGTCTCTCTCTCTCTCTCTCTCT 571  
Db 432 ACCAGGTGTGACAGAGAGAGAGATGCAAGCTGTCTCTCTCTCTCTCTCTCTCTCT 491  
QY 572 TGTGAGGTGTGACCGCAAGAGCAAGAGGTGTCTAGACTCCAAAGTGTGACTGTGAC 631  
Db 492 TGTGAGGTGTGACCGCAAGAGCAAGAGGTGTCTAGACTCCAAAGTGTGACTGTGAC 551  
QY 632 CATCTCAGGCGCTGTGACTGAGCGCGCTGTCTGCAAGCGGCTGTCACTGAGAGCG 691  
Db 552 CATCTCAGGCGCTGTGACTGAGCGCGCTGTCTGCAAGCGGCTGTCACTGAGAGCG 611  
QY 692 CTGTGATAGGTGTGACAGGTTACTATCACTGGATGGGGAAGCCCTGAGGCTGTAC 751  
Db 612 CTGTGATAGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671  
QY 752 CCAGTGTGTTTGTATGAGGCAATTCGCGAGCTGTGACAGAGCTGTGGGAGTCAAGT 811  
Db 672 CCAGTGTGTTTGTATGAGGCAATTCGCGAGCTGTGACAGAGCTGTGAGAGTCAAGT 731  
QY 812 TAAATATATCT 871  
Db 732 TAAATATATCT 791  
QY 872 GTTCCTGCAAAAGTGTGACAGTGTGACAGCGGCAATGGGATATTTTGTGCTAGAG 931  
Db 792 GTTCCTGCAAAAGTGTGACAGTGTGACAGCGGCAATGGGATATTTTGTGCTAGAG 851  
QY 932 ATCAGACCTGTCTATTTTGTAGCTCTGCGCAAAATTTCTTGGAATCAAGAGTGA 991  
Db 852 ACTGATATCTGTCTATTTTGTGCTCTGCGCAAAATTTCTTGGAATCAAGAGTGA 911  
QY 992 CGGCAAAAGCTTATCTTTGACTACCGTGTGATAGGAGGAGGACACCATCTGCCA 1051  
Db 1051 CGGCAAAAGCTTATCTTTGACTACCGTGTGATAGGAGGAGGACACCATCTGCCA 1051

Db 912 TGGGCAAAAGCCTGTCTTTGTGACTACCGTGTGACAGAGAGGAGGACACCATCTGCCA 971  
QY 1052 TGAGTGATCTCTGGAAGGTCTGTGTGACGAGTACAGAGCTCCCTGATGCACTTACCA 1111  
Db 972 TGATGTATCTCTGGAAGGTCTGTGTGACGAGTACAGAGCTCCCTGATGCACTTACCA 1031  
QY 1112 GACACTGCTTGTGAGTACCAAGAGTACATTCATTCAGATTAATGAATCCCAAGCAG 1171  
Db 1032 GACACTGCTTGTGAGTACCAAGAGTACATTCATTCAGATTAATGAATCCCAAGCAG 1091  
QY 1172 TAAATGAGCCCCAGCTAAAGTATCTTGAATGTGAGAGTGTGCTGGGAACTCACA 1231  
Db 1092 TAAATGAGCCCCAGCTAAAGTATCTTGAATGTGAGAGTGTGCTGGGAACTCACA 1151  
QY 1232 CCTCGGATCCGAGCTTACATTCAGAGATACAGTGGGATGTGACAAAGTGAAGCTT 1291  
Db 1152 CCTCGGATCCGAGCTTACATTCAGAGATACAGTGGGATGTGACAAAGTGAAGCTT 1211  
QY 1292 GATTTGAGCCCCGCTTCTGTGAGGCCAGCGCCCTGGGTTGAAATGTGTATGCC 1351  
Db 1212 GATTTGAGCCCCGCTTCTGTGAGGCCAGCGCCCTGGGTTGAAATGTGTATGCC 1271  
QY 1352 TGTGAGTACAAAGGAGAGTGTCTGCAAGATGTGTCTCGGCTACAAAGATTTAC 1411  
Db 1272 TGTGAGTACAAAGGAGAGTGTCTGCAAGATGTGTCTCGGCTACAAAGATTTAC 1331  
QY 1412 CAGACTGGAGCCTTTTGGACACCTGTATTCATGTACATGCCAAAGGAGGAGGCTGCA 1471  
Db 1332 GAGACTGGAGCCTTTTGGACACCTGTATTCATGTACATGCCAAAGGAGGAGGCTGCA 1391  
QY 1472 TCCAGACACAGAGACTGTACTCAGGAGATGAGAACCTGATCCCTGTGATGTCTGA 1531  
Db 1392 TCCAGACACAGAGACTGTATTCATGAGGAGATGAGAACCTGATCCCTGTGATGTCTGA 1448  
QY 1532 CTGCCCCATGTGTTTCTTCAACAGATTCACAAAGACCCCGGAGCTGCAAGCCGCTG 1591  
Db 1449 CTGCCCCATGTGTTTCTTCAACAGATTCACAAAGACCCCGGAGCTGCAAGCCGCTG 1508  
QY 1592 TCGCAATGGGTTTGTAGCGCTCGTATGCTCGAGAGAGAGAGGTTGGTCAATTAATG 1651  
Db 1509 TCAATAGGAGGTTGAGCTGTCTGTATGATTCGGAACAGGAGAGGTTGGTCAATTAATG 1568  
QY 1652 CCCCAGGAGTCACTGAGTGTGCGCTGTGAGCTGTGTGATGCTATTTTGGGAGCC 1711  
Db 1569 CCCCAGGAGTCACTGAGTGTGCGCTGTGAGCTGTGTGATGCTATTTTGGGAGCC 1628  
QY 1712 CTTGCGGAGAGTGTGCGGAGTGTGAGGCTTGTGACGCTGTGTAGTCAACAAAGTGTG 1771  
Db 1629 CTTGCGGAGAGTGTGCGGAGTGTGAGGCTTGTGACGCTGTGTAGTCAACAAAGTGTG 1688  
QY 1772 CCTAGTGTGCGGAGAGTGTGAGGCTGTGAGGAGGAGTGTGTGAAGTGCATTCACAA 1831  
Db 1689 CCTAGTGTGCGGAGAGTGTGAGGCTGTGAGGAGGAGTGTGTGAAGTGCATTCACAA 1748  
QY 1832 CACAGCTGGGTTCACTGTGACAGTGTGCAAGAGGAGGCTATGAGGAGCCGTTGGCTCC 1891  
Db 1749 CACAGCTGGGTTCACTGTGACAGTGTGCAAGAGGAGGCTATGAGGAGCCGTTGGCTCC 1808  
QY 1892 CAATTCAGACAAAGTGTGAGGCTGTGACAGTGTGCAAGGAGGCTGTGAGGCTGTG 1951  
Db 1809 CAATTCAGACAAAGTGTGAGGCTGTGACAGTGTGCAAGGAGGCTGTGAGGCTGTG 1868  
QY 1952 GTGTGAGAGTGTGAGGAGTGTGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGCA 2011  
Db 1869 GTGTGAGAGTGTGAGGAGTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGCA 1928  
QY 2012 TGGGCACTGACAGCTGTGAGGCTGTGATATATCAAGTGAAGTTGATGATGATGAT 2071  
Db 1929 TGGAGCAAT---CAGCTGTGAGGCTGTGATATATCAAGTGAAGTTGATGATGATGAT 1985  
QY 2072 TATGCAAGAGTCCAGATCTGTGAGGAGGCTGTGATGAGGAGGCTGTGAGGAGGCT 2125  
Db 1986 TATGCAAGAGTCCAGATCTGTGAGGAGGCTGTGATGAGGAGGCTGTGAGGAGGCT 2045



OY	2126	AGTACCACCAAGAGCTGGAAAGGAGGATGACAGAGGCTGACAGAGCCCTTGGGACAT	2185
Db	2046	AGTACCTCATACAGAGCTGGAAAGGAGGATGACAGAGGCTGACAGAGCCCTTCAGGACAT	2105
OY	2186	TCGTGAGAAAGCCAGATTTCCAAAGATGCTTTAGATCTTCAATCTCCGGTGGCCAA	2245
Db	2106	TCTGAGAGATGCCCCGATTTTCGAAAGTGCTAGCAGATCCCTTGCTCCAGTTGGCCAA	2165
OY	2246	GGCAAGGAGCTCAAGGATTAAGTACCTCCGGAGCCGCTGATATACCTCAAGATGACTGTGA	2305
Db	2166	GGTGGAGGCCCAAGGAACACTACCAAGACCGGCTGGATGACCTCAAGATGACTGTGA	2225
OY	2306	AAGAGTTCCGGCCCTGGGACAGTACAGTATCAGAACCCAAAGTTGAGTATCTCCAGGCTCAT	2365
Db	2226	AAGAGTTCCGGCCCTGGGAGTACAGTATCAGAACCCAAAGTTGAGTATCTCCAGGCTCAT	2285
OY	2366	CACATCAGATGGCGCTGAGGCTTGAGAGAAAGTGAGGCTTCCTGCACAAACACCAACATTC	2425
Db	2286	CACATCAGATGGAGCTGAGGCTTGAGAGAAAGTGAGGCTTCCTGCACAAACACCAATTC	2345
OY	2426	TCCTTCAGAGCACTACGTGGGGCCAAATGGCTTTAAAAGTGTGGGTCCGAGAGGCCACAG	2485
Db	2346	TGCCTCAGAGCCACTACGTGGGGCCAAATGGCTTTAAAAGTGTGGGTCCGAGAGGCCACAG	2405
OY	2486	ATTGGACAGACCCATGTTCAATCAGTACGCCAGTACATGGAGCACTGGCCAAAGAAACCA	2545
Db	2406	ATTAGCAGAAAGCCACGTGTGAGTACAGCCAGTACATGGAGCACTGCACAAAGGAAATCGA	2465
OY	2546	GGAGATTTCCAAAGGCTGATGTACAGTGTGCGGGAGGCTGTGCAGAGAAAGAG-----G	2595
Db	2466	GGACTATTTCCAAACAGAGCCCTCTCACTGTGTGGCAGAGGCCCTGTGATGAAGAGATGTGAG	2525
OY	2600	CGGAAGCGGACCGTGGACGGAGCCGTGTGCCAAAGGCTTGTGGGAAAATTGCAGAAAC	2655
Db	2526	CGGAAGCGGATAGCCCGGAGCGGTGTGTGTGCCAAGGCGTTGTGGAAAATTGCAGAAAC	2585
OY	2660	TAAATCTCTGGCCCCAGAGTGTGTGAGGAGAGGCCACGCAAAACCAATGAGAAAGAGATAG	2715
Db	2586	CAGATCCTCTGGCCCCAGAGTGTGTGACAGGAGGAGCCACTCAACCGGAAATTGAAGCAGATAG	2645
OY	2720	GCTTTATCAGCATAGTCTCCACCTTCTCAATTCGTGTCTAGATTCAGGAGAGTCAATGA	2775
Db	2646	GCTTTATCAGCAGATGCTCCGCTCTCTGATTAAGTGTCTCCGCTTCAGGGAGTCAAGTA	2705
OY	2780	TCAGTCCCTGCAAGG---AGAAGCAGAGAGGCTCAGACAAAAAGCTGATTTCTCTCAAA	2835
Db	2706	TCAGTCCCTTGAAGGAGGAAAGCAAAAGGATCAAAAACCGGATTCACCTCTCAAG	2765
OY	2837	CCGTGTGACTAAGCATATGATGATGATTCAACACAGCTGCACAAAGCAATCGGAAACTGGGA	2896
Db	2766	CCGTGTAAACAGGACATATGATGATGATTCAACACAGCTGCACAAAGCAATCGGAAACTGGAA	2825
OY	2887	AGAAAGAAACCCGCGACGCTTTACAGAAATGAAAAGATGGAGACAGACATCAGATCAGCT	2956
Db	2826	AGAAAGAACACAGCAGCTCTTACAGAAATGAAAAGTGGGAGAGAAATCAGATCAGCT	2885
OY	2957	GCTTTCCCGTCCCAACCTTGTAAAGCAGAGCCCAAGAACACATAGTATGGGCATATGC	3016
Db	2886	GCTTTCCCGTCCCAATCTTGTAAAGCAGAGCCCAAMGAACACCTGATATGGGCATATGC	2945
OY	3017	CACTTTTTATGAAGTTGAGAACATCTTAAAGATCTCAGAGAGTTTGACCTGCAGAGTTGG	3076
Db	2946	CACTTTTTATGAAGTTGAGACATCTTAAAGACCTCGAGAGATTTGACCTGCAGAGTTGA	3005
OY	3077	AGATAAAAAGACAGAAAGCTGAAAGAGCCATGAAAGACTCTCTACATCAGCCAGAAAGT	3136
Db	3006	CAACAGAAAACCAAAAGCTGAAAGAGCCATGAAAGACTCTCTACATCAGCCAGAAAGT	3065
OY	3137	TGCAGAGTCCAGTGAACAAGAGAGCAAGCAGAAAGCAGCCCTGGGAGAGCTGTGCTCGCA	3196
Db	3066	TTTCAGATGCCAGTACAAAGACCCACAGCAAGCAGAAAGAGCCCTGGGAGAGCTGTGCTCGCA	3125

OY		3197	CGCCCAAGGGGCGAAAGATGCAGCAGAGAGGCCCTGGAGATCTGTGGCAATGAGAACA	3256
Dd		3126	TGCACAGAGGCGAANAAGATTGGGGCCGGGAGAGCCCTGGAAATCTTCAGGTGAATTGANCA	3185
OY		3257	GGAGATNAGAGTGTGAACCTTGGAAGCCAAATGTGACACAGATGGAGCCTTGGCCATGGA	3316
Dd		3186	GGAGATTGGGAGTCTGNAACCTTGGAAGCCAAATGTGACACAGATGGAGCCTTGGCCATGGA	3245
OY		3317	GAAAGGACTGGCCACTCTGAAAAGTAGATGAGAGAAAGTGGAAAGAGAGCTGTCAAGGA	3376
Dd		3246	AAAAGGACTGGCCCTCTCTGAAAGATGAGATGAGGAAGTGAAGAGAGAGCTGGAAGGAA	3305
OY		3377	GGAGCAGAGATTGTGACATGATGATGGAAGCAGTGCAGATGGTTAAATTGCGAGAGGCCAAAG	3436
Dd		3306	GGAGCTGAGATTGTGACACGAATTAAGATGTCAGTACAGATGGTATTACAGAGAGCCCAAGA	3365
OY		3437	AGTTGAAMAACAGAGCCAAAGAAATGCTGAGATTACGATCCAGACACACTCAACACATTGGA	3496
Dd		3366	GGTTGATATCCAGAGCCAAAGAACGCTGGGGTTACAAATCCAACACACTCAACACATTAGA	3425
OY		3497	TGSCATCTCACCTAATAAG	3516
Dd		3426	CGGCCTCCTCATCTGATGG	3445
RESULT 12				
AL	AAL42911			
ID	AAL42911	standard; cDNA; 4316 BP.		
XX	AAL42911;			
AC				
XX				
DT	05-AUG-2002	(first entry)		
DE	Laminin gamma-2 chain cDNA sequence 2.			
KW	Laminin gamma-2; gene; ss; cancer; laminin gamma-2 chain inhibition;			
KX	carcinogen inhibition; anti-gamma-2 chain antibody;			
XX	epithelial cell adhesion; laminin-5.			
OS	Unidentified.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	118..3453		
FT		/tag= a		
FT	sig_peptide	/product= "Laminin gamma-2 chain 2"		
FT		118..183		
FT		/tag= b		
FT	mat_peptide	184..3450		
FT		/tag= c		
FT		/note= "Mature laminin gamma-2 chain 2"		
XX				
PN	US2002052307-A1.			
PD				
DD	02-MAY-2002.			
XX				
PF	08-JAN-2001; 2001US-0756071.			
XX				
PR	07-JAN-2000; 2000US-175005P.			
PR	04-OCT-1994; 94US-0317450.			
PR	18-FEB-1997; 97US-0800593.			
PR	15-SEP-2000; 2000US-0663147.			
XX				
PA	(TRYG/) TRYGVASON K.			
PA	(KALL/) KALLUNKI P.			
PA	(PYKE/) PYKE C.			
XX				
FL	Trygvason K, kallunki P, pyke C;			
XX				
DR	WPI; 2002-434824/46.			
DR	P-PSDB; AAO14993.			
XX				
FT	Modulating laminin 5 gamma 2 chain interactions of invasive carcinogens			
FT	for treating cancers and promoting attachment of cultured cells in			



1869 ATGTGCAAGTGAAGGACCTGTGTTGCAAGCCAGGATTTGGGCCCACTGAGCA 1928  
 2012 TGGGCACTGACCACTGTCACCTGCTATTAATCAAGTGAAGTTCAGATGATGATG 2071  
 1929 TGGAGCACTT---CAGCTGTCACCTGCTATTAATCAAGTGAAGTTCAGATGATG 1985  
 2072 TATGCAAGCACTGCAAGTCCCTGAGGCGCTGATTTGGAAGCTCAGG-----TGA 2125  
 1986 TATGCAAGCACTGCAAGTTCAGAGATGAGGCGCTGATTTGGAAGCTCAGGCGCT 2045  
 2126 AGTACCAAGCAAGCAAGTTCAGAGATGAGGCGCTGATTTGGAAGCTCAGGCGCT 2185  
 2046 AGTACCAAGCAAGCAAGTTCAGAGATGAGGCGCTGATTTGGAAGCTCAGGCGCT 2105  
 2186 TCTGAG 2245  
 2106 TCTGAG 2165  
 2246 GGCAG 2305  
 2166 GGTGAG 2225  
 2306 AAGAGTTCGGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2265  
 2226 AAGAGTTCGGGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2285  
 2366 CACTGAG 2425  
 2286 CACTGAG 2345  
 2426 TCTGAG 2485  
 2346 TGCCTGAG 2405  
 2486 ATTGAG 2545  
 2406 ATTGAG 2465  
 2546 GAGATATTCAG 2599  
 2466 GAGATATTCAG 2525  
 2600 CGAAG 2659  
 2526 CGAAG 2585  
 2660 TAAATCTGAG 2719  
 2586 CAAATCTGAG 2645  
 2720 GTCTTATCAAGATAGTCTGACCTGCTCAATTCGATTCAGATTCAGATTCAGATTC 2779  
 2646 GTCTTATCAAGATAGTCTGACCTGCTCAATTCGATTCAGATTCAGATTCAGATTC 2705  
 2780 TCAATCTGAG 2836  
 2706 TCAATCTGAG 2765  
 2837 CCGTGTGAGATCAAGATAGTCTGACCTGCTCAATTCGATTCAGATTCAGATTCAG 2896  
 2766 CCGTGTGAGATCAAGATAGTCTGACCTGCTCAATTCGATTCAGATTCAGATTCAG 2825  
 2897 AGAAG 2956  
 2826 AGAAG 2885  
 2957 GCTTTCCTGAG 3016  
 2886 GCTTTCCTGAG 2945  
 3017 CACTTTTATGAAGTGAAG 3076

2946 CACTTTTATGAAGTGAAG 3005  
 3077 AGATTAAG 3136  
 3006 CAAAG 3065  
 3137 TGAAGTGCAG 3196  
 3066 TTAAGATGCAG 3125  
 3197 CGGCAAG 3256  
 3126 TGAAG 3185  
 3257 GGAAGATAG 3316  
 3186 GGAAGATAG 3245  
 3317 GAAGGAG 3376  
 3246 AAG 3305  
 3377 GGAAG 3436  
 3306 GGAAG 3365  
 3437 AGTTGAAG 3496  
 3366 GGTGATACAG 3425  
 3497 TGGATCTTACAG 3516  
 3426 CGGCTTCCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3445

RESULT 13  
 AAC83733  
 ID AAC83733 standard; cdna; 5159 BP.  
 XX  
 AAC83733;  
 XX  
 02-MAR-2001 (first entry)  
 XX  
 DE Mouse laminin 5 cDNA, SEQ ID NO: 33.  
 XX  
 KW Mouse; laminin 5; vulnery; antilucer; antiinflammatory; antidiabetic;  
 KW cell adhesion promoter; wound healing; ulcers; burn; skin graft;  
 KW periodontitis; gingivitis; Type I diabetes; angiogenesis regulation; ss.  
 XX  
 OS Mus musculus.  
 XX  
 WO200066731-A2.  
 XX  
 PD 09-NOV-2000.  
 XX  
 XX  
 XX 28-APR-2000; 2000MO-US11459.  
 XX  
 XX 30-APR-1999; 99US-0131720.  
 XX 21-AUG-1999; 99US-0149738.  
 XX 24-SEP-1999; 99US-0155945.  
 XX  
 XX (BIOS-) BIOSATUM INC.  
 XX  
 XX Boutaud A;  
 XX  
 XX WPI; 2000-687538/67.  
 XX P-PSDB; AAB48472.  
 XX  
 XX Laminin 5-expressing cells, used to accelerate wound healing associated  
 XX with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,  
 XX burns, acute wounds and skin grafts -  
 XX  
 XX Claim 4; Page 213-219; 232pp; English.



OY	2103	ATTGGAAGGGCTCAGGGGTGGAGCAATACCACCAAGCG- - - - - AGCTGGAAAGGCAGG	2153
Db	1945	GTTTCAAAGGCTCAGGGTGTTGGTGTGTGTACAGTCCCATGTGCACCTTGGAAGGCCAG	2004
OY	2154	ATGCAGCAGGGTCAGCAGGCCCTTCGGGACAATTCTGAGAGAGAAGCCAGATTTCACAAGAT	2213
Db	2005	ATCGACGAGCTGAGCACAGGCCCTTCAGGACAATTCTGGGAGAAAGCTCAGATTTCGAAGGG	2064
OY	2214	GCTGTATATCTTCAATCTCCGGGTGGCCCAAGCAGGACTCAAGAAATAGCTACCCG	2273
Db	2065	GCAATGAAGGCCGTGGCTGTCTCGGCTGGCCCAAGGCACAGGACCAAGAAAGAACGACTACMAg	2124
OY	2274	GACCGCTCGATGACCTCAAGATGACGTGTGGAAAAGATTGGGGCCGTGGGACAGTACAGAT	2333
Db	2125	ACCGGCTCGATGACCTCAAGATGACGTGTGGAAAAGATTGGGGCCGTGGGACAGTACAGAT	2184
OY	2334	CAGAACCAAGTTCAGAGTACTCGCAGGCTCATCTACATGACGCTGAGCCTGGAGGAA	2393
Db	2185	CAGAACCAAGTTCAGAGTACTCGCAGGCTCATCTACATGACGCTGAGCCTGGAGGAA	2244
OY	2394	AGTAGGCTTCCCCTGCAAAACCAACAATCTCTCTCTTAAGGCACTACGTGGGCAAT	2453
Db	2245	AGCGAAGCTCTTGGAAAAACACAAATATTCATTCTTCTGAGCACTACGTGGGCGCAAT	2304
OY	2454	GCGTTTAAAGTCGGGCTCAGAGGCCCGAGATTTGGAGACACACAAATGTTCACTACGCC	2513
Db	2305	GATTTTAAAGTCGGGCTCAGAGGCCCGAGATTTGGAGACACACAAATGTTCACTACGCC	2364
OY	2514	AGTAACATGAGCAACTGGCAAGGAAACCAGAGATATTCCAAAGAGCTGATCTACTG	2573
Db	2365	AAGCAATGAGCAACTGCAAGGAAACCAGAGATATTCCAAAGAGCTGATCTACTG	2424
OY	2574	GTCGGCGAGGCTCTGCAAGGAGAGAGCGGCAAGCGGCACTGACCGGAGCCGTGTGCA	2633
Db	2425	GCCGCGAAGCTCTTGAAGTGAAGAGCGGCAAGTGGCTTGGGACAGCTCGTGGTACAA	2484
OY	2634	AGGCTTGGGAAAAATTSCAAAAACTTAACTCTGGGCCAGGAGTTGTCAGGAGAGGCC	2693
Db	2485	GGTCTTATGGGAAAAATTGAGAAAAACCAAGTCCCTGAGCCAGCAGCTCTATTGGAGGCG	2544
OY	2694	ACGCAAAACGACATGGAAGAGATAGTCTTATCAGCATAGTCTCCACCTTCTCAATTC	2753
Db	2545	ACCCAAAGCCGACATTTGAAGCTGATAGGCTGATCAGACAACTCTCCGCTCTGATTTCT	2604
OY	2754	GTCCTCGATTCAAGGGATCAATGATCAGTCTGTCAGAGTAAAGGAAGGAGGCTCAGA	2813
Db	2605	GCCTCTCAGCTTCAGGAGTCAATGATCTGCTTTCAGGTGGAAGCAAAAGGATCAGA	2664
OY	2814	CAAAAAGCTGATCTCTCTCAAAACCCTGTGACTAAGCATATGATGATTCACACAGT	2873
Db	2665	CAAAAAGCTGATCTCTCTCTCAAAACCCTGTGACTAAGCATATGATGATTCACACAGT	2724
OY	2874	CAAAAGCAATCTGGGAAACTGGGAAAGAAACCAGGAGCTCTTACAGATGGAAGAT	2933
Db	2725	CGAAAACAATCTGGGAAACTGGGAAAGAAACCAGGAGCTCTTACAGATGGAAGAT	2784
OY	2934	GGGAGACGACATCAGATCAGCTGCTTCCCGTGCACAACTTGTAAAGCAGAGCCCA	2993
Db	2785	AGGAGACGACATCAGATCAGCTGCTTCCCGTGCACAACTTGTGTAAAAACAGAGCCCA	2844
OY	2994	GAAACACTAAGTATGGGCAATGCCACTTTTTATNAAGTTGAACATCTTAAACATCTC	3053
Db	2845	GAAACACTAAGTATGGGCAATGCCACTTTTTATNAAGTTGAACATCTTGAACAACTC	2904
OY	3054	AGAGAGTTTGAACCTGCAAGTTGGAGATPAAAAGACAGAGAGCTGAAGAGCCATGAAGA	3113
Db	2905	CGAAGAGTTTGAATCTGCAAGTTGGAAGACAGAAAACAGAGGCTGAAGAGCCATGAAGA	2964
OY	3114	CTCTCCATCAATCAGCCAGAAAGTTGCAAGTGGCCAGTACAAAGAGCAAGCAAGCAAGCA	3173
Db	2965	CTCTCTCTATTTAGCCAGAAAGTTGCGGATGCCAGTACAAAGACCCAGCAAGCAGAAAGC	3024

OY		3174	GCCCTGGGCAATGTGTCGCGGCCAGACGCCCAAGGGGCAAAAGATTGCAGCAGGAGGACCTTG	3233
Dd		3025	GCCCTGGGAGACGCCACTGCTGCCAACCACGGGCAAGAAGCCAGCTTAGGGAGGCGCTTG	3084
OY		3234	GAGATCTCTGCGCAAGATAGAACAGAGAGATAGAGAGTGTGAACCTTGGAAGCCAAATGTGCACA	3293
Dd		3085	GAGATTCAGCACGAGATATGAGACTGTGAGATATAGGAGTTGTGAACCTTGGAAGCTTAATGTGCACA	3144
OY		3294	GCAGATGAGACCTTTGGCCCATGTGAGAGAGGAGCTGCGCCACTCTGAAAAGTGAATGAGAGAA	3353
Dd		3145	GCAGATGGGGGCGCTTGCGCCATGTGAAGAAAGGGAGCTCCCACTCTGGAAGAGGAGATGAGAGAG	3204
OY		3354	GTGGAAGSAGAGCTGTGTAAGGAAGAGAGAGAGTGTGATGATGATGATGAGATGAGACGAGTGCAG	3413
Dd		3205	ATG---ATTGAGCTGTGGCCAGAAAGAGAGCTGGAGTTTGACACGGATTAAGACACGGTGCAG	3261
OY		3414	ATGGTAAATTGCGAGAGGCCCAAAAGAGTTGAAACAGAGCCAGACCAAGATGCTGAGTTACGATC	3473
Dd		3262	CTGGTGAATTACTGAAAGCCCAACAGCTGATGTCCAGAGGACACGAGATGCCGGAGTTACCATC	3321
OY		3474	CAGAACACACTCAACACATTTGGATGGCATCTCTACACCTAATAGACACAGCTGCGACGTGTG	3533
Dd		3322	CAAGACACRCTCAACACATTTGGAGCGCATCTACACCTCATAGACACAGCTGCGCAGTGTG	3381
OY		3534	GATGAAGAGAGGCTGATCTTACTGTGAGACAGAAAGCTTTCCGAGCCAAAGACTCAGATCAAC	3593
Dd		3382	GATGAAGAGAGGATGATGATCTTGAAGAACMAAGGGCTTTCCAAAGCCAAAGACCCCAATCAAC	3441
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Dd		3442	AGTGGACTTGGGCGCTTGATGTCTGACCTGAGAGAGAGGGTGCCTCGGACAGAGAACCCAC	3501
OY		3654	CTCCGTTTCCTGAGAGACTAGCATGATGGATGGGATTTCTGGCTGATGTGAAGAAACCTTGAAGAAC	3713
Dd		3502	CTCCATCTGCTGGAGACTAGCATGATGAAATTTCTGCTGATGTGAAGAAACCTTGAAGAAC	3561
OY		3714	ATCAGGAGCAACCTGCCCCGGGSGTGTCTACAAATCCCAAGGCTCTTGAGCAACAAGTGAAC	3773
Dd		3562	ATTGGAAGCAACCTGCCCCAGGCGTGTCTACAAATCCCAAGGCTCTTGAGCAACAAGTGAAGT	3621
OY		3774	TGCCTTAGAGATTCTCTCAAC	3793
Dd		3622	TGTCTATAGAGATTGTCTCAC	3641
<hr/>				
RESULT 14				
ID	AAD31144	standard; cDNA; 3579 BP.		
XX	AAD31144;			
XX				
DT	21-AUG-2002	(first entry)		
XX				
DE	Mouse laminin gamma2 chain cDNA.			
XX				
KW	Cancer; cell proliferation; integrin receptor; signalling pathway;			
RN	gene therapy; mouse; laminin gamma2; ss.			
XX				
OS	Mus sp.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	1..3579		
FT		/*tag^a		
XX		/product= "Laminin gamma2 chain"		
EN	WO200230465-A2.			
PD	18-APR-2002.			
PF	12-OCT-2001; 2001WO-US32127.			
XX				
RR	12-OCT-2000; 2000US-239705P.			
RR	24-OCT-2000; 2000US-242812P.			







XX 30-APR-1999; 99US-0131720.  
PR 21-AUG-1999; 99US-0149738.  
PR 24-SEP-1999; 99US-0155945.  
XX  
PA (BIOS-) BIOSTATUM INC.  
XX  
PI Boulard A;  
XX WPI: 2000-687538/67.  
DR P-PSDB; AAB46473.  
XX  
XX Laminin 5-expressing cells, used to accelerate wound healing associated  
PT with diabetic foot ulcers, venous ulcers, pressure sores, skin surgery,  
PT burns, acute wounds and skin grafts -  
XX  
XX Claim 4; Page 223-228; 232pp; English.  
XX  
XX The present sequence encodes a laminin 5 chain polypeptide. Recombinant  
CC laminin 5-expressing cells are used to accelerate wound healing,  
CC especially diabetic foot ulcers, venous ulcers, pressure sores, skin  
CC surgery, burns, acute wounds, skin grafts, corneal ulcerations,  
CC gastro-intestinal ulcers, periodontitis, and gingivitis. They are also  
CC used to improve the biocompatibility of medical devices, and to promote  
CC cell adhesion to a surface. They can be used for the ex vivo treatment  
CC of Type I diabetes. Laminin can also be used to regulate angiogenesis.  
CC The cell line produces and secretes recombinant heterotrimeric laminin,  
CC whereas prior art cell lines have been created that produce but do not  
CC secrete only one or two chain laminins.  
XX  
SQ Sequence 5057 BP; 1318 A; 1231 C; 1343 G; 1164 T; 1 other;  
Query Match 63.6%; Score 2537.4; DB 21; Length 5057;  
Best Local Similarity 83.0%; Pred. No. 0;  
Matches 2944; Conservative 1; Mismatches 582; Indels 18; Gaps 4;  
QY 261 ACCTCCGGAGGAAGTCTGTGATGCAACGGAGATCCAGCAATGCATCTTGACAG 320  
DB 1 ACCCTCAGAGGGAAGTCTGTGATGCAATGGAAATCCAGGCATGTGTTTGATCAG 60  
QY 321 GAACCTCACAAGACAGCAAGAAATGATTCGCTGCTCAACTGCATGACACACTGAT 380  
DB 61 GAGCTCCATCGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
QY 381 GGCATCCACTCGAGAGGTGCAAGGAGGATTTACGACAGAGAGAGAGAGAGAGGAG 440  
DB 121 GGGGTTCACGCGAGCGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
QY 441 TTACCTGCAATTTGTAAGTCTCTTAGCGCTGATGACACTGTGACAGG 500  
DB 181 CTACCTGCAACTGCACTCAAAAGGTTCCCTCAGTGTGATGTGACAACTCTGACAA 240  
QY 501 TGCAGCTGTAAAGGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 560  
DB 241 TGCAGGTGTAAAGGTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
QY 561 ACACTCACTGATGCTGGGTGCGCCCAAGACCAAGAGGCTGCTAGACTCCAACTGTG 620  
DB 301 ATGCTCAACGATGTGATGACCCGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
QY 621 GACCAGCTGCACTGCAAGGCGCTGTGACTCAGGCGGCTGTGCTGCAACCGGCTGTC 680  
DB 361 GACCAGCTGCACTGCTGACACCTGTGATTTCTGGCGATGTGCTGCAAAACGACGTC 420  
QY 681 ACTGGAGAGCGCTGTGATAGGTGTGACAGAGGTTACTATCACTGTGATGGGAAACCT 740  
DB 421 ACTGGAGAGCGCTGTGATAGGTGTGACAGAGGTTACTATCACTGTGATGGGAAACCT 480  
QY 741 CAGGCTGTACCACTGTTTTTGTATGAGGATTCGCGACAGCTGCAAGAGCTCTGGGAC 800  
DB 481 GAGGCTGTACCACTGTTTTTGTATGAGGATTCGCGACAGCTGCAAGAGCTCTGGGAC 540  
QY 801 TACAGTGTCAATAATCATCTGCTTCCATCAAGATGTGATGAGCTGGAAGGCTGTC 860

DB 541 TTGAGTGTCCAAATAACACTTCAACTTTCAGTGTGAGATGTGATGGTGGAGCGGT 600  
QY 861 CAAGAAAGAGGTTCTCTGCAAGACTCCAGTGTGACAGGCGCATGCGATATTTTAC 920  
DB 601 CAGAGAAAGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660  
QY 921 TCAGCAGAGATCAGAGCCGCTGATTTGTACTCTGCGCAATTTCTGGAAATCA 980  
DB 661 TCTGCCGAGAGATAGACCCGCTGATTTGTGAGGCGCCCTGCAATTTCTGATACAG 720  
QY 981 CAGGTGAGTACGAGGCAAGGCTATCTTTGACTACCGCTGTGATGAGGAGGAGGAGC 1040  
DB 721 CAAGTGAATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780  
QY 1041 CCATCTGCCATGACGATGATCTGTGAAAGGTCTGTGATGATCAGATCCTCTGATG 1100  
DB 781 CCGTCTGCTACGATGATGATCTGTGAAAGGTCTGTGATGATCAGATCCTCTGATG 840  
QY 1101 CCATCTGAGACAGACAGGAGGCTGTGAGGATCAGAGAGCTTACATTCAGATTAATGAA 1160  
DB 841 GCTCAGGAGAGACATTCCTCTGTGAGATCAGAGAGCTTACATTCAGATTAATGAA 900  
QY 1161 CATCCAAAGCACTAATTTGAGAGGCGCCAGCTAAGTATTTGATGAGGAGGAGGAGG 1220  
DB 901 CATCCAAAGCACTAATTTGAGAGGCGCCAGCTAAGTATTTGATGAGGAGGAGGAGG 960  
QY 1221 AACCTCAGAGC--CTGCGGATCCGAGTACTTACGAGAGATACAGTACTGAGTAT 1277  
DB 961 AACCTCAGAGCCTTCTGATGATCCGAGTACTTACGAGAGATACAGTACTGAGTAT 1020  
QY 1278 GACAAAGTACCTGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1337  
DB 1021 GATTAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
QY 1338 CAATGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1397  
DB 1081 CGTGTGATGATCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140  
QY 1398 AAAAGAGTATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1457  
DB 1141 AAAAGAGTATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
QY 1458 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1517  
DB 1201 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1259  
QY 1518 CCTGAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1577  
DB 1260 --TGAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1317  
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DB 1318 AAGCGATGTGCTGTGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1377  
QY 1638 GTGTGCAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1697  
DB 1378 GTGTGTAACAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1437  
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Db 1618 GACCATGTCCTCCCAACCCAGACAGACAGTGTGAGCTTGCATCTGCAATGCGAGCCCCCAGGGT 1617  
QY 1938 TCGGAGCCTGTGAGTGTCCAGAGTGTAGTGCAGCTGTGTGTTGCAAGCCAGGCTTGTGTGC 1997  
Db 1678 GCGGAGCTGTGAGTGTGTGAGGTGATGGCAGCTGTGTGTTGCAAGCCAGGCTTGTGTGC 1737  
QY 1998 CTGACGTGTAGCATGGGCGACTGACAGCTGTCCAGCTTGTATTAATCAAGTGAAGTT 2057  
Db 1738 TTCAACTGTATCAGCGAGCCCTAACCGATTGTCTGCTTGTATCAATCAAGTGAAGATT 1797  
QY 2058 CAGATGATCATGTTTATGACAGCTCCAGATCCCTGAGGCCCCGATTGTGAAGGCTCAG 2117  
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QY 2229 AATCTCCGGTGGCCAGAGGAGCTCAGAGATACAGAGATACCGGGAGCGCTGATGAC 2288  
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QY 2469 GCTCAGAGGCGCAGAGATTTGAGAGAGCCAGTGTTCAGTCCAGCAATGAGAGCA 2528  
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QY 2709 GAGCAGATGATGCTTATCAGAGATGCTCCACCTCTCAATTCGCTGTCAGATTCAG 2768  
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QY 2949 GATCAGCTGCTTCCGTCGCAACCTTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3008  
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QY 3009 GGCATATGCCATTTTATGAGTGTGAGAAACATCTTAAAGATCTCAGAGATTTGACCTG 3068  
Db 2758 GGCATATGCCATTTTATGAGTGTGAGAAACATCTTAAAGATCTCAGAGATTTGACCTG 2817  
QY 3069 CAGTGTGAGATTAAG 3128  
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QY 3549 ATCTTATGAG 3608  
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QY 3609 TTGATGAG 3668  
Db 3355 TTGATGAG 3414  
QY 3669 ACTAGATAGATGAGATTTGCTGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3728  
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QY 3729 CCCCCGGGCTGCTACAAATACCCAGGCTCTTGAGCAACAGTGAAGCTGCTTACAGATTTC 3788  
Db 3475 CCCCCGGGCTGCTACAAATACCCAGGCTCTTGAGCAACAGTGAAGCTGCTTACAGATTTC 3534  
QY 3789 TCAAC 3793  
Db 3535 TCCAC 3539

Search completed: July 6, 2003, 04:31:04  
Job time : 811 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 04:09:53 ; Search time 5205 Seconds  
(without alignments)  
12411.873 Million cell updates/sec

Title: US-10-053-662a-1

Perfect score: 3989  
Sequence: 1 tgggtccctctattcacag.....ccagataatgcttatttg 3989

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: \*  
1: em\_estba: \*  
2: em\_esthum: \*  
3: em\_estlin: \*  
4: em\_estlinu: \*  
5: em\_estloy: \*  
6: em\_estlpl: \*  
7: em\_estiro: \*  
8: em\_hlc: \*  
9: gb\_estl: \*  
10: gb\_est2: \*  
11: gb\_hlc: \*  
12: gb\_est3: \*  
13: gb\_est4: \*  
14: gb\_est5: \*  
15: em\_estfun: \*  
16: em\_estom: \*  
17: gb\_gss: \*  
18: em\_gss\_hum: \*  
19: em\_gss\_inv: \*  
20: em\_gss\_pln: \*  
21: em\_gss\_vit: \*  
22: em\_gss\_fun: \*  
23: em\_gss\_mam: \*  
24: em\_gss\_mus: \*  
25: em\_gss\_other: \*  
26: em\_gss\_pro: \*  
27: em\_gss\_rnd: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	621	15.6	769	12 BG679084 602627037
2	609.4	15.3	919	12 BG679408 602627409
3	603.8	15.1	973	14 BQ687091 BQ687091
4	586.8	14.7	872	14 BQ686460 BQ686460
5	582	14.6	1007	12 BG749494 BG749494
6	562.8	14.1	782	12 BG679991 BG679991

	7	530	13.3	763	13	B1149191
	8	524.2	13.1	936	12	BG175669
	9	517.2	13.0	674	9	AL710184
	10	516.6	13.0	645	12	BG423903
C	11	499.4	12.5	962	9	AT701039
	12	493.8	12.4	687	12	BE744593
	13	489	12.3	791	13	BG918341
	14	488.2	12.2	774	12	BF163600
	15	485.4	12.2	730	12	BG676601
	16	475.8	11.9	796	13	BM047745
	17	475.6	11.9	760	10	BB627917
	18	472.2	11.8	938	12	BF302784
	19	471	11.8	661	13	B1082572
	20	459.8	11.5	763	10	B114962
	21	456.4	11.4	978	12	BF100494
	22	456.2	11.4	667	10	BB617855
	23	450.8	11.3	626	14	BM849299
C	24	447	11.2	617	12	BF081464
	25	442.6	11.1	538	10	BE032523
	26	442.4	11.1	596	13	BM538716
	27	435.6	10.9	561	12	BF564481
	28	429.2	10.8	536	13	BM044707
C	29	414.8	10.4	624	10	BE005892
	30	407.2	10.2	819	13	B1691847
	31	406.2	10.2	656	10	BE311555
C	32	401.6	10.1	507	10	AW369523
	33	398	10.0	697	12	BF320138
	34	386.2	9.7	590	14	BQ335079
C	35	385.6	9.7	549	12	BF149296
	36	381.2	9.6	466	12	BF045508
C	37	367.8	9.2	729	14	BM980789
	38	367	9.2	572	12	BF815018
C	39	365.8	9.2	460	12	BE814142
	40	362.2	9.1	502	12	BF750814
	41	354.8	8.9	512	14	BQ312520
C	42	346.6	8.7	458	12	BF747980
	43	344.8	8.6	404	12	BF874660
C	44	341.2	8.6	447	12	BE813970
	45	341	8.5	457	14	BM836374

#### ALIGNMENTS

RESULT 1  
LOCUS BG679084 769 bp mRNA EST 01-MAY-2001  
DEFINITION 602627037F1 NCI\_CGAP\_Skn4 Homo sapiens CDNA clone IMAGE:4752080 5',  
mRNA sequence.  
ACCESSION BG679084  
VERSION BG679084.1 GI:13910481  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 769)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaaps-remail.nih.gov  
Tissue Procurement: James Cleaver, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNI)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMNI at:  
http://image.lnl.gov  
Plate: LHAM10609 Row: 1 Column: 09  
High quality sequence stop: 768.  
Location/Qualifiers  
1. 769  
FEATURES  
source

[illegible]

DEFINITION	602627409p1.NCI_CGAP_Skn4.Homo sapiens cDNA clone IMAGE:4752266.5, mRNA sequence.
ACCESSION	BC679408
VERSION	BC679408.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo 1 (bases 1 to 919)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:rsrausb@mail.nih.gov">rsrausb@mail.nih.gov</a> Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL), DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> plate: L1AM10610 row: a column: 03 High quality sequence stop: 843. Location/Qualifiers 1..919 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4752266" /clone_lib="NCI_CGAP_Skn4" /tissue_type="squamous cell carcinoma" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI CGAP Library." 1 others
BASE COUNT	261 a 198 c 282 g 177 t
ORIGIN	
Query Match	15.3%; Score 609.4; DB 12; Length 919;
Best Local Similarity	87.9%; Pred. No. 3.2e-146;
Matches 664; Conservative 0; Mismatches 91; Indels 0; Gaps 0;	
QY	3083 AAGAGCGAACCTTAAGAGCGCTCAAGAGAGCTCTCTACATTCAGCCAGAGTTGAGG 3142
DB	2 AAAAGCGAAGACTTAAGAGCATTGAGAGAGCTCTCTACATTCAGCCAGAGTTTACGA 61
QY	3143 TGCCAGTGACAAAGACGAAGCAAGCAGAGCAGCCCTGGGCGAGTCTGTCGCCAGCCCA 3202
DB	62 TGCCAGTGACAAAGACCCAGCAAGCGAGAAAGAGCCCTGGGAGCGCTGCTGTGATGCACA 121
QY	3203 GAGGCGAAGATGACGACGACGAGGAGGCCCTTGGAATCTCTGCGAAGATAGAACGAGAT 3262
DB	122 GAGGCGAAGAGATGGGGCCGGGGAGGCCCTTGGAATCTCCAGTAGATTCAGAGAGAT 181
QY	3263 AGGAGGTCGTAACCTTGGAGGCCATGTGACAGCAGATGAGACCTTGGCCATGAGAAAGG 3322
DB	182 TGGGAGTGTGAACCTTGGAGGCCATGTGACAGCAGATGAGACCTTGGCCATGAGAAAGG 241
QY	3323 ACTGCGCACTCTGAAAAGTGAGATGAGAGAAGTGAAGAGAGAGCTGTCAAGAGAGACA 3382
DB	242 ACTGCGCTCTCTGAAAAGTGAGATGAGAGGAAGTGAAGAGAGAGCTGTGAAAAGAGAGCT 301
QY	3383 GGACTTTGACATGATATGAGCGAGAGTGAGATGATGTAATTCAGAGGCCCAAGAGTTGA 3442
DB	302 GGAGTTTTCACACGATATGATGATGACATGATGATGATGATGATGATGATGATGATGATG 361
QY	3443 AAACAGAGCCAGAGATGCTGAGATTAGATCAAGACACACTCAACACTTGGATGGCAT 3502
DB	362 TACAGAGCCCAAGAGCGCTGGGGTTTAACTCCAAAGACACACTCAACACTTGAACGGCT 421
QY	3503 CCTACACCTAATAGACCAAGCTGGCAGTGTGATGAAGAGGCTGATCTTACTGAGACA 3562

Db 422 CCGATCTGATGACACGCTCTCAGTAGATGAGAGAGGGGCTGCTTACTGAGACA 481  
OY 3563 GAAGCTTTCCGAGCCAGACTCAGATCAACAGCCAGCTTGGATGTCAGACT 3622  
Db 482 GAAGCTTTCCGAGCCAGACTCAGATCAACAGCCAGCTTGGATGTCAGACT 541  
OY 3633 GGAAGAGAGGACATGCGGAGAGAGGGCCACTCCCTTCTGAGACTAGATGATG 3682  
Db 542 GGAAGAGAGGACATGCGGAGAGAGGGCCACTCCCTTCTGAGACTAGATGATG 601  
OY 3683 GATTCGTGCTATGTAAGAAACCTGAGAACATCAGGACCACTGCCCCGGCTGCTA 3742  
Db 602 GATTCGTGCTATGTAAGAAACCTGAGAACATCAGGACCACTGCCCCGGCTGCTA 661  
OY 3743 CAATACCCAGGCTCTTGAACAAGTGAAGCTGCTAGATTTCTACCAAGGCTCT 3802  
Db 662 CAATACCCAGGCTCTTGAACAAGTGAAGCTGCTAGATTTCTACCAAGGCTCT 721  
OY 3803 TGGGATTGAGACCTAGCTGCTTGAAGATTCTCTCA 3837  
Db 722 TGGGATTGAGACCTAGCTGCTGAGGAGCCATGTCTA 756

RESULT 3  
B0687091 973 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8034003 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6208015  
DEFINITION 5' mRNA sequence.  
ACCESSION B0687091  
VERSION B0687091.1 GI:21812420  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 973)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CM2365 row: a column: 08  
High quality sequence stop: 694.  
Location/Qualifiers  
1..973  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6208015"  
/clone\_lib="NIH\_MGC\_110"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI;  
Site\_2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

BASE COUNT 289 a 217 c 279 g 179 t 9 others  
ORIGIN

Query Match 15.1%; Score 603.8; DB 14; Length 973;  
Best Local Similarity 82.4%; Pred. No. 9.4e-145;  
Matches 740; Conservative 0; Mismatches 147; Indels 11; Gaps 4;

OY 2110 AGGCTCAGGTGAGACAGTACCCAGCAGAGCTGGAAGCAGAGATGACGAGCTGAGC 2169  
Db 2 AGGCTGAGATGAGATACCTGATACAGAGCTGGAAGCAGAGATGACGAGCTGAGC 61  
OY 2170 AGGCTTGGGACATTTCTGAGAGAGAGCCAGATTTCAAGAGATCTTGTAGATCTTCA 2229  
Db 62 AGGCTTGGGACATTTCTGAGAGAGATGAGATTTCAAGAGATCTTGTAGATCTTCA 121  
OY 2230 ATTCCTGGGTTGGCCAGGCAAGGACTCAAGAAATAGTACCGGAGCCGCTGATGAGC 2289  
Db 122 GTCTCAGTTGGCCAGGTTGAGAGAGCCCAAGAAATAGTACCGGAGCCGCTGATGAGC 181  
OY 2290 TCAAGATGACTGTGGAAGAGAGTTCGGGCTGCGGACATGATGAGAACCAAGTTTCAG 2349  
Db 182 TCAAGATGACTGTGGAAGAGAGTTCGGGCTGCGGACATGATGAGAACCAAGTTTCAG 241  
OY 2350 ATACTGCAAGGCTCATCACTCAGATGCGCTGAGCCTGAGAGAAAGTAAAGCTTCCGTC 2409  
Db 242 ATACTGCAAGGCTCATCACTCAGATGCGCTGAGCCTGAGAGAAAGTAAAGCTTCCGTC 301  
OY 2410 AAAACACCAATCTCTCCTTCAGGACCTAGTGGGCGCAAAATGGCTTAAAGTCTGG 2469  
Db 302 GAAACACTACATTTCTGCTGCTGAGACCACTAGTGGGCGCAAAATGGCTTAAAGTCTGG 361  
OY 2470 CTCAGAGGCGCAGAGATTGGCAGACACCATGTTCACTCAGCCAGTAACTGAGACAC 2529  
Db 362 CTCAGAGGCGCAGAGATTGGCAGACACCATGTTCACTCAGCCAGTAACTGAGACAC 421  
OY 2530 TGGCAAGGAAACCCAGAGATTTTCCAAAGAGCTGATGCTACTGTGCGGAGGCTCTGC 2589  
Db 422 TGACAAAGGAAACTGAGACTATTCACAAAGCCCTCTCACTGTGCGGAGGCGCTTGC 481  
OY 2590 AGGAGGAG-----GCGGAAGCGGACCTGTGAGAGGAGCCGTGTGCAAGAGCTTGG 2643  
Db 482 ATGAAGGAGTGGGAAGCGGAGAGCGGTACCCGAGGCTGTGTGTGCAAGGCTTGG 541  
OY 2644 GAAATTTCCAGAAACTAAATCTTGGGCCAGAGATTTGCGAGGAGGCCACCAACCG 2703  
Db 542 AAAAAATTGAGAAAAACAAGTCCCTGCGCCAGATTTGACAAAGGAGGCCACTCAAGCG 601  
OY 2704 ACATGAGACAGATAGTCTTATTCAGCATCTCCACCTTCTCAATTCCGTCTCAGA 2763  
Db 602 AAATGAGACATATAGTCTTATTCAGCATCTCCACCTTCTCAATTCCGTCTCAGA 661  
OY 2764 TTCAGGAGTCAATATATAGTCTTCCAGCT---AGAAGCAGAGGCTCAGACAAAAG 2820  
Db 662 TTCAGGAGTCAATATATAGTCTTCCAGGAGTGAAGACANAGAGATCAAAAG 721  
OY 2821 CTGATTTCTCTCAAAACCGTGTGACTAAGCATATGATGATGATTCAGACGCGCAAGCA 2880  
Db 722 CGGATTTCACTTCTCAAGCTTGTGATACCCAGGACATATGATGATTCAGACGCGCAAGCA 781  
OY 2881 ATCTGGGAATCTGGAAGAAAGAACCCGCGACCTCTTACAGATGGAAGAAATGG- GAGA 2939  
Db 782 ATCTGGGAATCTGGAAGAAAGAACGACAGACACTTCTACAGATGGAAGAAATGGGNGAGA 841  
OY 2940 CAGACATGATGATCACT-CTTTCCCTGTCGCACTTGTCTAAACCAAGCCCAAGAA 2996  
Db 842 GAGAAATGATGATCACTGCTTCCCTGTCGCACTTGTCTAAACCAAGCAAGCAAGAA 899

RESULT 4  
B0686460 872 bp mRNA linear EST 15-JUL-2002  
LOCUS AGENCOURT 8064560 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6206340  
DEFINITION 5' mRNA sequence.  
ACCESSION B0686460  
VERSION B0686460.1 GI:21811776  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 872)	NIH-MGC	<a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact:	Robert Strausberg, Ph.D.		

FEATURES	Location/Qualifiers
source	1. .872

BASE COUNT	258 a	197 c	257 g	159 t	1 others
ORIGIN					

Oy	2644	GAAATTCGACAAAACCTAAATCTCTGGCCGAGAAATTTGCAGGAGGCGACGCAAAACCG	2703
Db	542	AAAAATTGGAAAAACCAAGTCCTCGGCCACAGCACTTACAAAGGAGGCCACTCAAGGG	601
Oy	2704	ACATGGAAAGCAGATAGTCTTATACAGCATAGTCTCACCTTCTCAATTCCGTGTCTCAGA	2763
Db	602	AAATTTGAAGCAGATAGTCTTATACAGCACACTCTCCGCTCTCGATTCAAGTGTCTCGCG	661
Oy	2764	TTCAAGGGGTCATATGATCAGTCTCTTGCAGGT---AGAAAGGCAAGAGCGTCGACACAAAAG	2820
Db	662	TTTCAGGAGGTACAGTATAGTCTCTTTCAGGTGGGAAGAACCAAGAGGATCCAAACAAAAG	721
Oy	2821	CTGATTTCTCTCYCAAAACCGTGTGACTAAGCATATGATGATGAGTTCAAGCAGCTGCACAAGCA	2880
Db	722	CGGATTTCACTCTCAAGCCTCGGTAAACAGCAGCATATGAGATGAGTTCAACGCTACACAGAGA	781
Oy	2881	ATCA-GGGAAACTGGGAAGAAACCCGGAGGCTTACAGAAATGGAAAGAAATATGGGGA	2939
Db	782	ATCTGGGAAACTGGAAAGAAAGACACAGACGCTTTACAGAAATGGAAAGAAATGTGGGA	841

RESULT	5
LOCUS	BG749494
DEFINITION	BG749494 1007 bp mRNA linear EST 15-MAY-2001 60270762/F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4844167 5' , mRNA sequence.
ACCESSION	BG749494
VERSION	BG749494.1 GI:14060147
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

FEATURES	Location/Qualifiers
source	1. .1007

BASE COUNT	232 a	270 c	309 g	196 t
ORIGIN				





QY 1899 GCAGACAAGTGTGAGCTTGGCAACTGCAACCCAGTGGGCTCGAGGCTGTGAGTGTGCA 1958  
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Db 537 GCAGACAAGTGTGAGCTTGGCAACTGCAACCCAGTGGGCTCGAGGCTGTGAGTGTGCA 596  
QY 1959 AGTGATGGCAGCTGTGTTTGGCAAGCCAGGCTTGTGGGCTC-AGCTGTGAGATGCGGC 2017  
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Db 597 AGTGATGGCAGCTGTGTTTGGCAAGCCAGGATTTGTGGGCTCCCAACTGTGAGCATGAGC 656  
QY 2018 ACTGACACAGCTGTGCTGCTATATATCAAGTGAAGTTCAGATGATCAG-TTATGTC 2076  
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Db 657 ATT---CAGCTGTGCAAGCTTGTCTATATATCAAGTGAAGTTCAGATGATCAGTTTATGC 713  
QY 2077 AGCAGCTCCAGATCTGAGAGCCCTGATTTGCAAGGCTCAGGCTGAG 2124  
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Db 714 AGCAGCTCCAGATGAGAGGCGCTGATTTCAAGGCTCAGGCTGAG 761  
RESULT 7  
B1149191 763 bp mRNA linear EST 05-JUL-2001  
LOCUS 602848711F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:5012330 5',  
DEFINITION B1149191  
ACCESSION B1149191 GI:14609192  
VERSION B1149191.1 GI:14609192  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 763)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
http://image.llnl.gov  
Plate: LLAM1063 row: e column: 03  
High quality sequence stop: 753.  
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/tissue\_type="spontaneous tumor, metastatic to mammary.  
Stem cell origin."  
/lab\_host="DH10B"  
/note="Organ: Lung; Vector: PCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"  
BASE COUNT 236 a 179 c 214 g 134 t  
ORIGIN  
Query Match 13.3%; Score 530; DB 13; Length 763;  
Best Local Similarity 82.7%; Pred. No. 9.8e-126;  
Matches 630; Conservative 0; Mismatches 130; Indels 2; Gaps 2;

QY 2624 CGTGTGCAAAAGGCTTGTGGGAAAATTCAGAAAACCTTAATCTTGCCAGAGATTGTC 2683  
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Db 122 CGTGTGCAAAAGGCTTATGGAATAATTAGGAAAACCAAGTCCCTGAGCAGAGCTGTGC 181  
QY 2684 GAGGAGGCGCCAGCAAAACCGACATGGAAGCAGATAGCTTTATCAGATAGTCTCAGCT 2743  
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Db 182 AAGGAGGCGCCAGCAAAACCGACATGGAAGCAGATAGCTTTATCAGATAGTCTCAGCT 241  
QY 2744 TCTCAATTCGCTGCTCAGATTGAGGAGTGCATGATGATGCTCTTCAGGTAGAACGAA 2803  
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Db 242 CCTAGATTGCTGCTCTCAGCTTTCAGGAGTGCATGATGATGCTCTTCAGGTAGAACGAA 301  
QY 2804 GAGGCTCAGACAAAAGCTGATTTCTCTCAAAACGCTGTGACTTAAGCATATGATGAGTT 2863  
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Db 302 GAGGATCAGACAAAAGCTGATTTCTCTCAAAACGCTGTGACTTAAGCATATGATGAGTT 361  
QY 2864 CAAGCAGCTGCAAAAGCAATCTGGGAACCTGGGAAGAAACCCGCGACGCTCTTACAGAA 2923  
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Db 362 CACGCGTGTGCGAAACATCTGGGAACTGGGAAAGAAACAGGACGCTTACAGAC 421  
QY 2924 TGGAAAGATGGGAGACAGACATCAGATCAGCTGCTTCCGCGCAACCTTGCTTAAAG 2983  
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Db 422 TGGAAAGATGGGAGACAGACATCAGATCAGCTGCTTCCGCGCAACCTTGCTTAAAG 481  
QY 2984 CAGAGCCCAAGAAAGCACTAAGTATGGGCAATGCCACTTTTATGAAGTTGAGAACATCTT 3043  
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Db 482 CAGAGCCCAAGAAAGCACTAAGTATGGGCAATGCCACTTTTATGAAGTTGAGAACATCTT 541  
QY 3044 AAGAAATCTCAGAGATTTGACCTGCAAGTGTGAGTAAAGGCAAGGCTGAACAGG 3103  
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Db 542 GAAGAACTCTCCGAAATTTGATGTGAGTGAAGACAGAAAGGCAAGGCTGAACAGG 601  
QY 3104 CATGAAGAGACTCTCTACATCAGCCAGAAAGTTGAGGTCGACGACGACGACGACGAC 3163  
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Db 602 CATGAAGAGACTCTCTACATCAGCCAGAAAGTTGAGGTCGACGACGACGACGACGAC 661  
QY 3164 AGCAG-PAAGAGCCCTGGGCGAGTGTGCTGCGCAGCCCGACAGAGGCAAGATGACAGCA 3222  
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Db 662 AGCAGAAAAGCGCCCTGGGCGAGCGCCAGCCGACACACAAAGGCAAGAAAGCGAGCTA 721  
QY 3223 GGGAGGCGCTGCG-AGATCTCTGCGCAATGAAACAGAGATA 3263  
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Db 722 GGGAGGCGCTGGAAGATCAGACGAGATGACGAGAGATA 763  
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LOCUS 602334661F2 NCI\_CGAP\_Mam1 Mus musculus cDNA clone IMAGE:4457942 5',  
DEFINITION B6175669  
ACCESSION B6175669  
VERSION B6175669.1 GI:12682372  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 936)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
http://image.llnl.gov  
Plate: LLAM10255 row: 1 column: 15  
High quality sequence stop: 681.

FEATURES  
source

Location/Qualifiers  
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/note="Organ: mammary; Vector: pCMV-Sport6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

BASE COUNT 273 a 234 c 295 g 134 t

ORIGIN

Query Match 13.1%; Score 524.2; DB 12; Length 936;  
Best Local Similarity 82.0%; Pred. No. 3.5e-124;  
Matches 652; Conservative 0; Mismatches 138; Indels 5; Gaps 4;

2887 GAACTGGGAGAGAAACCCGGCAGCTCTTACAGATGGAAGATGGGAGACACAT 2946  
1 GGAACCTGGGAGAGAAACACGCGACTTTTACAGACGAAAGATGAGACGACCTT 60  
2947 CAGATCAGCTCTTCCCGTCCCAACCTTGTAAAGAGAGCCCAAGACCACTAAGTA 3006  
61 CAGATCAGCTCTTCCCGTCCCAACCTTGTAAAGAGAGCCCAAGACCACTAAGTA 120  
3007 TGGGCAATGCCATTTTATGAGTTGAGAACATCTTAAAGATCTCAGAGATTGACC 3066  
121 TGGGCAATGCCATTTTATGAGTTGAGAACATCTTAAAGATCTCAGAGATTGACC 180  
3067 TGGGCAATGCCATTTTATGAGTTGAGAACATCTTAAAGATCTCAGAGATTGACC 3126  
181 TGGGCAATGCCATTTTATGAGTTGAGAACATCTTAAAGATCTCAGAGATTGACC 240  
3127 GCCAGAAAGTTGAGAGTCCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3186  
241 GCCAGAAAGTTGAGAGTCCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
3187 CTCTGCGGAGCGCCAGAGGAGCAAAAGATGACAGCCAGAGAGAGAGAGAGAG 3246  
301 CCAGTCCGAGACCTTACGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
3247 AGATGAGACAGAGATGAGAGTCTGAACTTGAAGCCAAATGTGACAGATGAGAGCT 3306  
361 AGATGAGACAGAGATGAGAGTCTGAACTTGAAGCCAAATGTGACAGATGAGAGCT 420  
3307 TGGCCATGAGAGAGAGTGGGCACTTGAAGAGTGAAGTGAAGAGAGAGAGAGAG 3366  
421 TGGCCATGAGAGAGAGTGGGCACTTGAAGAGTGAAGTGAAGAGAGAGAGAGAG 480  
3367 TGTCAAGAGAGAGAGAGTGTGACATGATGATGAGAGAGAGAGAGAGAGAGAG 3426  
481 TGGCCATGAGAGAGAGTGTGACATGATGATGAGAGAGAGAGAGAGAGAGAGAG 540  
3427 AGGCCCAAGAGTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3486  
541 AAGCCCAAGAGTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
3487 ACACATGAGAGAGAGTGTGACATGATGATGAGAGAGAGAGAGAGAGAGAGAG 3546  
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3607 CCTTATGAGAGAGAGTGTGACATGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 3666  
716 CCTTATGAGAGAGAGTGTGACATGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 775

QY 3667 AGACTAGCATAGATG 3681  
DB 776 GAACACCGAGATTTG 790

RESULT 9  
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LOCUS  
DEFINITION DKFZp686J1267.1 686 (synonym: h1cc3) Homo sapiens cDNA clone  
ACCESSION AL710184  
VERSION AL710184.1 GI:19693539  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 674)  
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann  
S.  
EST (Duesterhoeft, et al.)  
Unpublished (1995)  
COMMENT Contact: Duesterhoeft A  
MIPS  
Am Klopferplatz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp686J1267) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source

Location/Qualifiers  
1. .674  
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/lab\_host="DH10B"  
/note="Vector: pT7-1; Site\_1: SfiI; Site\_2: SfiI;  
CDNA-collection"

BASE COUNT 146 a 190 c 204 g 132 t 2 others

ORIGIN

Query Match 13.0%; Score 517.2; DB 9; Length 674;  
Best Local Similarity 88.3%; Pred. No. 1.9e-122;  
Matches 597; Conservative 0; Mismatches 70; Indels 9; Gaps 3;

114 ACAGCGGAGCGGAGAGTGAAGAACTCCAGCGGAGGCGCGGAGAGAGAGAGAGAG 169  
2 ACAGCGGAGCGGAGAGTGAAGAACTCCAGCGGAGGCGCGGAGAGAGAGAGAGAG 59  
170 --CAGCGGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 227  
60 GAGACGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 119  
228 TGTCTTCTGCT 287  
120 TGTCTTCTGCT 179  
288 AACGGGAAGTCCAGCAATGATCTTTGACAGCAAGTTCACAAACAGACAGAGAAATGA 347  
180 AATGGGAAGTCCAGCAAGTGTATCTTTGATCGGAACTTCACAAACAGTGTATATGA 239  
348 TTTCT 407  
240 TTTCT 299  
408 GGATTTTACAG 467

Db	300	GGCTTTTACCGGCACAGAGAAAGGACCGCTGTTGGCCCTGCAATTGTAACGCCAAAGT	359
QY	468	TCTCTTACGCTCCATGTGACAACTCTGGACGGTCCAGCTGTAAAGCCAGGTGTACAGA	527
Db	360	TCTCTTAATGCTCGATGTGACAACTCCGAGCGTCCACTGTAAACCAAGTGTGACAGA	419
QY	528	GACAGGTGACCCGATGCTGTGCCCCGCTTCCACACATCACTGATGATGGGGTGGCCCCA	587
Db	420	GCCAGATCGAACCCATGTCTGTGCGACAGCTTCCACATGCTCAGCGATGGGGGTGACCCAA	479
QY	588	GACCAAAAGGCTGTAGACTCCAAAGTGTGACTGTGACCCAGCTGGCATCTCAGGAGCCCTGT	647
Db	480	GACCAGAACTGTAGACTCCAAAGTGTGACTGTGACCCAGCTGGCATCGACAGGCGCTGT	539
QY	648	GACTCAGCGCGCTGTGTGCAAGCCGCGCTCACTGGAGAGCCGTGTGATAGGTGTGGA	707
Db	540	GACGCGGGCCCTGTGTGTGCAAGCCAGCTGTCACTGGAGAAAGCTGTGATAGGTGTGGA	599
QY	708	CCAGGTACTATCACTGATGGATGGGGAAACCTCAGGGCTGTACCACTGTTTTGCTAT	767
Db	600	TCAGTTCATTAATCTGGATGGGGGGAACCTGANGGCTGTA-CCAGTGTTCGTGCTAT	658
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Db	659	GGGCATTCCGCACGCT	674

RESULT 10					
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LOCUS	BG423903	945 bp	mRNA	linear	EST 14-MAR-2001
DEFINITION	60244854F1 NIH.MGC.14	Homo sapiens	CDNA	clone IMAGE:4588548	5',
	mRNA sequence.				

ACCESSION	BG423903
VERSION	BG423903.1
KEYWORDS	GI:13330409
SOURCE	EST.
ORGANISM	human.
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. . .	1 (bases 1 to 945)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Contact: Robert Strausberg, Ph.D.				

Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: DCD/DTP  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: L1CMI320 row: k column: 13  
High quality sequence stop: 668.

FEATURES	Location/Qualifiers
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/tissue_type="renal cell adenocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: kidney; Vector: pOT7; Site_1: XhoI, Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match	13.0%;	Score 516.6;	DB 12;	Length 945;
Best Local Similarity	83.6%;	Pred. No. 3.2e-122;		
Matches 648; Conservative	0;	Mismatches 114;	Indels 13;	Gaps 5

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Db	65	TTTGTGTGAACATGGCCGCCAGTGAAGGCTTTGTAGGCCCTGTCAATGACAAACAAATGTGAC	124
QY	1773	CCATGTGGCTCCGGGAAATGTGACCGCGCTGACAGGACAGGTGTCAATGTCATCCCAAC	1833
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QY	1833	ACAGCTGGGGTCACTGTGACCAAGTGAACAGAGGCTACTATGTGGGAGCCCGTTGGCTCCC	1893
Db	185	ACACCCGGGCATCTACTGTGGACCAAGTGAACAGAGGCTACTTTCGGGGAGCCCAATTTGGCTCCC	244
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QY	1953	TGTGAAGTGTGAGCAGCTGTGTTTGTGCAAGCAGGCTTTGGTGGCCTCAGCTGTGAGCAT	2017
Db	305	TGTGAAGTGTGAGCAGCTGTGTTTGTGCAAGCAGGATTTGGTGGCCCAACTGTGAGCAT	364
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QY	2247	GCAAGGACTCAGAGAAATAGCTTACCCGGGAGCCGCTGATGTGACTCAAGATGACTGTGAA	2308
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QY	2365	TCACTCAGATGCGCCTCAGGCTGGAAGAAATGAGGCTTCCTCCGCAAAACACCA	2419
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VERSION	AI701039.1
KEYWORDS	GI:4988939
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ORGANISM	human.
	Homo sapiens
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 662)
AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .



QY 1883 GTTGGCTCCCAATCCAGCAGACAGATGTGCACTGGCACTGCCAGTGGGCTCGA 1942  
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 QY 2063 GGAATCAATTTATCCAGCAGCTCCAGATCTGAGAGCCCTGATTTGCAAGGCTCAGG 2119  
 Db 479 GGAATCAATTTATCCAGCAGCTCCAGATCTGAGAGCCCTGATTTGCAAGGCTCAGG 538  
 QY 2120 ---TGGAGCAGTCCCAATCCAGCAGACAGATGTGCACTGGCACTGCCAGTGGGCTCGA 2176  
 Db 539 TGAATGAGATGTGCAAGTATGAGCAGCTGTGTTGCAAGCCAGGCTTGTGCTCAG 597  
 QY 2177 TCGGAGCATTTCTAGAGAGAGCCAGATTTTCAAGATGCTGTTAGATCTTCAATCTCCG 2236  
 Db 598 TCGAGCATTTCTAGAGAGAGCCAGATTTTCAAGATGCTGTTAGATCTTCAATCTCCG 657  
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 Db 658 GTTGG---CAAGGTGAGAGCCAGAGAGAGCAGC 687  
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 ORGANISM Mus musculus  
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 791)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-r@mail.nih.gov  
 Tissue Procurement: Jeffrey Green M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
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 Library constructed by Life Technologies. Investigator  
 providing samples: Jeffrey Green, M.D., NIH"  
 BASE COUNT 226 a 190 c 231 g 144 t

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 Db 122 CTGGCCCAAGCAAGAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181  
 QY 2297 GACTGTGGAAGAGTTGGGCTGAGGAGTCAATGATGATGATGATGATGATGATGAT 2356  
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 QY 2357 CAGGCTATCATCAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2416  
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 QY 2477 GCGCAGAGATTTGGCAG 2536  
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 QY 2537 GGAAGCCAGAGATTTCAAG 2596  
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 QY 2597 AGGCGAG 2656  
 Db 482 AGGCGAG 541  
 QY 2657 AACTAAATCTCTGAGCCAG 2715  
 Db 542 AAGCAAGATCTCTGAGCCAG 601  
 QY 2716 ATAGGCTTATAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2775  
 Db 602 ATAGGCTTATAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 QY 2776 ATGATCAGTCTTGGCAGGT-AGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2834  
 Db 661 GTGATCTGTCCTTCAAG 720  
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 SOURCE house mouse.  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 774)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM9198 row: j column: 21  
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 Matches 623; Conservative 0; Mismatches 149; Indels 6; Gaps 4;

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 QY 2725 ATCAGCATAGTCTCACCCTTCTCAATTCCTGTCAGATTCAGGAGTCAATGATCAGT 2784  
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 QY 3205 GGGCAAGAGATGAG 3264  
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 ORGANISM Homo sapiens

REFERENCE  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 930)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: James Cleaver, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM10599 row: k column: 19  
 High quality sequence start: 6  
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FEATURES  
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 /note="Organ: skin; Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCL.CGAP library."

BASE COUNT 298 a 199 c 277 g 156 t  
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Query Match 12.2%; Score 485.4; DB 12; Length 930;  
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 Matches 707; Conservative 0; Mismatches 171; Indels 19; Gaps 10;

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 DB 31 GGAAG 90  
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Db	151	GCTCTTACAGAAATGGAAAGATGGAGACAAATACAGATAGCTGCTTCCCGGCCAA	210
OY	2972	CCTTGCTTAAAGCAGAGCCCAAGAACGACTAAGTATGGGCAATGCCACTTTTATATGAAGT	3031
Db	211	TCTTGCTTAAAGCAGAGCACAAGAAAGCACTGATATGGGCATATGCCACTTTTATGAAGT	270
OY	3032	TGAGAACACTTTTAAAGAATCTCAGAGAGTTTGACCTGCAAGTTGGAGATTAAGACGAGA	3091
Db	271	TGAAGAGCACTCTTAAAAACCTCAAGAGATTTTGACCTGCAAGTTGACAAACAAAAAGCAGA	330
OY	3092	AGCTGAAGAGCCCATGAAGAGACATCTCCCTACATCAGCCAGAAAGGTTCGAGGTGCACAGA	3151
Db	331	AGCTGAAGAGCCCATGAAGAGACATCTCTTACATATACCCAGAAAGTTTTCAGATGCACAGGA	390
OY	3152	CAAGACGAAGCAACAGAACGACGCTTGGGCACTGCTGCTCCACAGCCCAAGAGGGCAAA	3211
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Db	451	GAATGGGGCCCGGAGGGCCCTGGAAATCTCCAGTAGAGATTTGAACAGAGAGATTTGGGGAGT	510
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Db	511	CTGAACCTTGGAAAGCCCATGTTACACAGCAGATGGAGCCCTTGGCCATGAGAAACGGGACCTGGC	570
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OY	3504	CTACACCTAATATAGACCAAGCCTGCGCAGTG----TGATGTAAGAGAGGCTGATCTTACTG	3558
Db	751	CTGCATAATTGATGAGCAGCTCTCAGTGTAGAGTAGAGCAGGGGCTGGCTATATACGTGG	810
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Db	811	AGCAGGAAGCTTTTCCGAGGCCAAGAGAGCAGATCAACAGCCACAGATGCGAGCCATGACAG	870
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Job time : 5211 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 6, 2003, 04:11:53 ; Search time 169 Seconds  
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7238.660 Million cell updates/sec

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Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2986.2	74.9	5200	US-08-800-593-12	Sequence 12, Appl
3	2956.4	74.1	5156	US-09-643-597-130	Sequence 130, App
4	2726	68.3	4316	US-08-317-450B-14	Sequence 14, Appl
5	2726	68.3	4316	US-08-800-593-14	Sequence 14, Appl
6	410.4	10.3	603	US-09-328-111-582	Sequence 582, App
7	388	9.7	551	US-09-328-111-448	Sequence 448, App
8	140.8	3.5	401	US-09-221-298-26	Sequence 26, Appl
9	79.2	2.0	7218	US-08-232-463-14	Sequence 14, Appl
10	71	1.8	6942	US-08-460-309-3	Sequence 3, Appl
11	71	1.8	6942	US-08-125-077-3	Sequence 3, Appl
12	53.6	1.3	1848	US-08-635-137-1	Sequence 1, Appl
13	53.6	1.3	1848	US-09-136-981-1	Sequence 1, Appl
14	50	1.3	1811	US-08-482-677-7	Sequence 7, Appl
15	50	1.3	2779	US-08-482-677-5	Sequence 5, Appl
16	50	1.3	2783	US-08-152-019A-41	Sequence 41, Appl
17	47.8	1.2	1921	US-08-482-677-3	Sequence 3, Appl
18	47.8	1.2	1926	US-08-152-019A-43	Sequence 43, Appl
19	47	1.2	1743	US-08-665-259-20	Sequence 20, Appl
20	47	1.2	1743	US-08-762-500-20	Sequence 20, Appl
21	47	1.2	1974	US-08-762-500-78	Sequence 78, Appl
22	45.2	1.1	2166	US-08-152-019A-42	Sequence 42, Appl
23	45	1.1	608	US-09-370-838-172	Sequence 172, App
24	42.4	1.1	3931	US-08-144-121-1	Sequence 1, Appl
25	42.4	1.1	3931	US-08-735-883-1	Sequence 1, Appl
26	40.6	1.0	468	US-08-600-982-29	Sequence 29, Appl
27	40.6	1.0	468	PCT-US94-10261A-29	Sequence 29, Appl

28	40.6	1.0	5496	US-08-600-982-23	Sequence 23, Appl
29	40.6	1.0	5496	PCT-US94-10261A-23	Sequence 23, Appl
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31	39.4	1.0	4534	US-08-935-450-1	Sequence 1, Appl
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33	39.2	1.0	6803	US-08-665-259-19	Sequence 19, Appl
34	39.2	1.0	6803	US-08-762-500-19	Sequence 19, Appl
35	38.6	1.0	289	US-09-007-005-17	Sequence 17, Appl
36	38.6	1.0	289	US-09-244-796-17	Sequence 17, Appl
37	38.6	1.0	1700	US-09-099-677A-4	Sequence 4, Appl
38	38.6	1.0	1700	US-09-261-471-4	Sequence 4, Appl
39	38.6	1.0	2065	US-08-335-8650-8	Sequence 8, Appl
40	38.4	1.0	2277	US-08-676-967-2	Sequence 2, Appl
41	38.4	1.0	2277	US-08-676-974-2	Sequence 2, Appl
42	38.4	1.0	2277	US-09-098-487-2	Sequence 2, Appl
43	38.2	1.0	440	US-09-221-298-81	Sequence 81, Appl
44	38.2	1.0	2963	US-09-232-200-60	Sequence 60, Appl
45	38.2	1.0	2963	US-09-232-197-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1  
US-08-317-450B-12  
Sequence 12, Application US/08317450B  
Patent No. 5660982  
GENERAL INFORMATION:  
APPLICANT: trygvasson, Karl  
APPLICANT: Kallunkl, Pekka  
TITLE OF INVENTION: Laminin Chains: Diagnostic and  
TITLE OF INVENTION: Therapeutic Use  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BANNER & ALLEGRETTI, LTD.  
STREET: Ten South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/317,450B  
FILING DATE: 04-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 94,778  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5200 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 118..183  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 118..3699  
FEATURE:  
NAME/KEY: polyA\_site  
LOCATION: 4433







1889 CCCCAGTGCCTCTGTGGGAATGTGACCCGCTGACAGGAGGAGGTGTGAAAGTGTATCCAAA 1748  
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1809 CAACCCAGCAGACAGAGTGTGAGCTTCACTGCACTGCAACCCAGTGGGCTGAGAGCTGTGA 1868  
1869 ATGTCGAGAGTGTGAGCTTGTGTCAGAGCCAGAGATTTGGTGGCCCACTGTGAGCA 1928  
2012 TGGGCACTGACAGCTGTGAGCTGTGATTAATCAAGTGAAGTGAAGTGAAGTGAAGTGA 2071  
1929 TGGAGCAATT--CAGCTGTGAGCTGTGATTAATCAAGTGAAGTGAAGTGAAGTGAAGTGA 1985  
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2126 AGTACCAAGCAGAGCTGAGAGCCAGAGATGACAGAGCTGAGAGGCTTCCGAGAT 2185  
2046 AGTACCTGATACAGAGCTGAGAGCCAGAGATGACAGAGCTGAGAGGCTTCCGAGAT 2105  
2186 TCTGAGAGAGCCAGATTTCAAGATTCGTGATAGATCCCTCAATCCCGGAGGCGCAA 2245  
2106 TCTGAGAGATGCCAGATTTCAAGATTTGATGAGATGATCCCTGATCCAGTGGCGCAA 2165  
2246 GGCAGAGACTCCAGAGATAGCTACCGGAGCCGCTGATGATGATGATGATGATGATGATG 2305  
2166 GGTGAGAGGCCAAGAGAGACACTACAGAGCCGCTGATGATGATGATGATGATGATGATG 2225  
2306 AAGAGTTCGGGCTTGGGAGTCACTATCAGAACCAAGTGAAGTGAAGTGAAGTGAAGTGA 2365  
2226 AAGAGTTCGGGCTTGGGAGTCACTATCAGAACCAAGTGAAGTGAAGTGAAGTGAAGTGA 2285  
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2286 CACTCAGATGCGCTGAGAGCCGAGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2345  
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2486 ATTGGCAGACAGCAGTGTTCAGTCAAGCCAGTAAATGAGAGTGAAGTGAAGTGAAGTGA 2545  
2406 ATTGGCAGACAGCAGTGTTCAGTCAAGCCAGTAAATGAGAGTGAAGTGAAGTGAAGTGA 2465  
2546 GGAGATATCCAAAGAGTGTGATGCTGAGTGGGAGGCTGAGAGGAGGAGGAGGAGGAGGAGG 2599  
2466 GGAGATATCCAAAGAGTGTGATGCTGAGTGGGAGGCTGAGAGGAGGAGGAGGAGGAGGAGG 2525  
2600 CGGAAGCGGAGCCTGAGAGGAGCCGTGTCAGAAAGCTGTGGGAAATTTGAGAGAAAC 2659  
2526 CGGAAGCGGAGCCTGAGAGGAGCCGTGTCAGAAAGCTGTGGGAAATTTGAGAGAAAC 2585  
2660 TAAATCTCTGCCCCAGAGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2719  
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2706 TCAGTCTCTGAGAGTGAAGAGAGAGAGAGAGATCAACAAAAGCGGATTCACCTCTCAAG 2765  
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2766 CCTGTATACAGAGGATATGATGATTCACAGCTGACACAAAAGATCTGGGAAACTGGA 2825  
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2826 AGAAGAAACCCGAGAGCTTATACAGATGAGAAAGATGGAGAGAGATGATGATGATGATG 2885  
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2886 GCTTTCCGTCACATCTTGTGTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2945  
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2946 CACTTTTATGATGATGAGAAATCTTAAAGATCTGAGAGATTTGATGATGATGATGATGATG 3005  
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3006 CACAGAAAGCAGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3055  
3137 TGCAGGTGCGCAGTACAG 3196  
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3126 TGCACAGAGGAG 3185  
3257 GGAGATGAG 3316  
3186 GGAGATGAG 3245  
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3437 AGTGAAG 3496  
3366 GGTGATATCAG 3425  
3497 TGGCATCTTACACCTAATAG 3556  
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3617 AGAGCTGGAAG 3676  
3546 AGAGCTGGAAG 3605  
3677 AGATGGAGTTCGGCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3736  
3606 AGATGGAGTTCGGCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3665  
3737 CTGCTCAATATCCAGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3796  
3666 CTGCTCAATATCCAGAGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3725  
3797 GGTCTTGGAGATGAG 3837  
3726 GGTCTTGGAGATGAG 3766

RESULT 3  
US-09-643-597-130  
; Sequence 130, Application US/09643597  
; Patent No. 6426072  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong













1532 CTGCCCATTTGGTTTCTACAAAGATTCACAAGACCCCGCAGCTGCAAGCCGCTCCCTG 1591  
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1509 TCATTAACGGGTTTCAAGCTGCTGATGATTCGAGACAGAGAGGTGTGTCAATTAATG 1568  
1652 CCCCCAGGTTGTCATGCTGCTGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1711  
1589 CCGTCCCGGGGTCAACGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1628  
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2766 CCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2825  
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2826 AGAAGAAACCCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2885  
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2886 GCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2945  
3017 CACTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3076  
2946 CACTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3005  
3077 AGATTAAG 3136  
3006 CACAGAAAG 3065  
3137 TGCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3196  
3066 TGCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3125  
3197 CGCCCAAG 3256  
3126 TGCAG 3185  
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3426 CGGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3445

RESULT 6  
US-09-328-111-582/c  
; Sequence 582, Application US/09328111  
; Patent No. 6262333  
; GENERAL INFORMATION:  
; APPLICANT: Endege, Wilson O.  
; APPLICANT: Steinhmann, Kathleen E.  
; APPLICANT: Astle, Jon H.

```

: APPLICANT: Burgess, Christopher C.
: APPLICANT: Bushnell, Steven E.
: APPLICANT: Carroll III, Eddie
: APPLICANT: Catino, Theodore J.
: APPLICANT: Dertli, Adnan
: APPLICANT: Ford, Donna M.
: APPLICANT: Lewis, Marcia E.
: APPLICANT: Monahan, John E.
: APPLICANT: Schlegel, Robert
: TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
: FILE REFERENCE: CCD-257 (US)
: CURRENT APPLICATION NUMBER: US/09/328,111
: EARLIER FILING DATE: 1999-06-08
: EARLIER APPLICATION NUMBER: US 60/088,801
: NUMBER OF SEQ ID NOS: 850
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 582
: LENGTH: 603
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(603)
: OTHER INFORMATION: n = A,T,C or G
US-09-328-111-582

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Query Match      10.3%  Score 410.4:  DB 4:  Length 603;
Best Local Similarity 88.3%:  Pred. No. 3.9e-108;
Matches 455:  Conservative 0;  Mismatches 59;  Indels 1;  Gaps 1;

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QY 752 CCAAGTCTTTTGGTATGGGATTCGCGACAGCTCCAGCTCTGGGAGTACAGTGTCCA 811
DB 515 CCGAGGTTCTGATAGGATTCAGCAAGTCCGAGTTNCGAATNCAAGTGTCCA 456
QY 812 TAAATATCTCTGCTCCCTTCATCAAGATGTGATGGCTGGAAGCGTGTCCAAAGAA 871
DB 455 TAAGATCACTTNTACCTTTCATCAAGATGTGATGGCTGGAAGCGTGTCCAAAGAA 396
QY 872 GTCCTCGCAAGAGCTCCAGTGTGTCACAGCG -CCATCGGATATATTAGTCCAGCAG 930
DB 395 GTCTCTCGCAAGAGCTCCAGTGTGTCACAGCGCCCATCAAGTGTGTTAGTCCAGCAG 336
QY 931 GATCAGACCTGTCTATTTTGTAGCTCTGCAAAATTTCTTGGAAATCAACAGGTAGCT 990
DB 335 GACTAGACCTGTCTATTTTGTAGCTCTGCAAAATTTCTTGGAAATCAACAGGTAGCT 276
QY 991 ACGGCAAAAGCTATCTTTGATCTACCGTGTGATAGGAGGAGCAGACACCATCTGCC 1050
DB 275 ATGGTCAAAAGCTGTCTCTTTGATCTACCGTGTGATAGGAGGAGCAGACACCATCTGCC 216
QY 1051 ATGACGATCTCTGAAAGGCTGTGCTAGTACAGTCCCTGATGCCACTTAGCA 1110
DB 215 ATATGATGATCTCTGAAAGGCTGTGCTAGTACAGTCCCTGATGCCACTTAGCA 156
QY 1111 AGACACTGCTCTGAAAGGCTGTGCTAGTACAGTCCCTGATGCCACTTAGCA 1170
DB 155 AGACACTGCTCTGAAAGGCTGTGCTAGTACAGTCCCTGATGCCACTTAGCA 96
QY 1171 GTAAATGAGAGGAGGAGTGTGCTAGTACAGTCCCTGATGCCACTTAGCA 1230
DB 95 ATAAATGAGAGGAGGAGTGTGCTAGTACAGTCCCTGATGCCACTTAGCA 36
QY 1231 CCTCGGATCGAGTACCTACGAGAAATACAGT 1265
DB 35 CCTCGGATCGAGTACCTACGAGAAATACAGT 1

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RESULT 7  
 US-09-328-111-448  
 : Sequence 448, Application US/09328111  
 : Patent No. 626233

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: GENERAL INFORMATION:
: APPLICANT: Endege, Wilson O.
: APPLICANT: Steinmann, Kathleen E.
: APPLICANT: Astle, Jon H.
: APPLICANT: Burgess, Christopher C.
: APPLICANT: Bushnell, Steven E.
: APPLICANT: Carroll III, Eddie
: APPLICANT: Catino, Theodore J.
: APPLICANT: Dertli, Adnan
: APPLICANT: Ford, Donna M.
: APPLICANT: Lewis, Marcia E.
: APPLICANT: Monahan, John E.
: APPLICANT: Schlegel, Robert
: TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
: FILE REFERENCE: CCD-257 (US)
: CURRENT APPLICATION NUMBER: US/09/328,111
: EARLIER FILING DATE: 1999-06-08
: EARLIER APPLICATION NUMBER: US 60/088,801
: NUMBER OF SEQ ID NOS: 850
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 448
: LENGTH: 551
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-328-111-448

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Query Match      9.7%  Score 388:  DB 4:  Length 551;
Best Local Similarity 84.6%:  Pred. No. 1e-101;
Matches 462:  Conservative 0;  Mismatches 75;  Indels 9;  Gaps 2;

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QY 2332 ATCAGAACCAAGTTCAGATATCTCGCAGGCTCATCACTAGATCCGCTGAGGCTGAG 2391
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QY 2392 AAAGTACGCTTCCTCTGCAAAACCAACATTCCTCTCTGACAGCACTACGTGGGCCAA 2451
DB 61 AAAGTACGCTTCCTCTGCAAAACCAACATTCCTCTCTGACAGCACTACGTGGGCCAA 120
QY 2452 ATGGCTTTAAAGTCTGGGCTCAGAGAGGCCAGGATTTGGCAGCAGCCATGTTCACTAG 2511
DB 121 ATGGCTTTAAAGTCTGGGCTCAGAGAGGCCAGGATTTGGCAGCAGCCATGTTCACTAG 180
QY 2512 CCAGTAACATGAGCAACTGCGCAAAAGAAACCCAGGAGTATTCCAAAAGAGCTGATGTCAC 2571
DB 181 CCAGTAACATGAGCAACTGCGCAAAAGAAACCCAGGAGTATTCCAAAAGAGCTGATGTCAC 240
QY 2572 TGGTGGCCAGGCTCTGCAAGAGAGG-----GCCGAAGCGGACCTGAGAGCGGCG 2625
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QY 2626 TGGTGGCAAGGCTCTGCGAAATTTGCAAAACTAAATCTCTGGCCAGGAGTGTTCGA 2685
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QY 2803 AGAGGCTCAGACAAAAGCTGATTTCTCTCAAAACCGTGTGACTAAGCATATGATGAGT 2862
DB 481 AGAGGCTCAGACAAAAGCTGATTTCTCTCAAAACCGTGTGACTAAGCATATGATGAGT 540
QY 2863 TCAAGC 2868
DB 541 TCAAGC 546

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RESULT 8  
US-09-221-298-26  
Sequence 26, Application US/09221298  
Patent No. 6284241  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS  
FILE REFERENCE: 210121.471  
CURRENT APPLICATION NUMBER: US/09/221.298  
CURRENT FILING DATE: 1998-12-23  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 26  
LENGTH: 401  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (219)  
OTHER INFORMATION: Where n is a, c, g or t  
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NAME/KEY: modified\_base  
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LOCATION: (325)  
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LOCATION: (374)  
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NAME/KEY: modified\_base  
LOCATION: (380)  
OTHER INFORMATION: Where n is a, c, g or t  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: (390)  
OTHER INFORMATION: Where n is a, c, g or t  
US-09-221-298-26

Query Match 3.5%; Score 140.8; DB 4; Length 401;  
Best Local Similarity 85.7%; Pred. No. 1.1e-30;

Matches 168; Conservative 0; Mismatches 27; Indels 1; Gaps 1;  
QY 3314 GGAGAGGGGACCTGCTGAAAGTGATGAGAGAGGAGGAGGCTGCTCAAG 3373  
Db 1 GGAAAAGGAGCTGGCCCTGCTGAAAGTGATGAGAGGAGGAGGAGGCTGCTCAAG 60  
QY 3374 GAAGGAGCAGAGTTGACATGATATGACGAGTCAGATGTAATTGACAGAGGCCA 3433  
Db 61 GAAGGAGCTGAGATTGACACGAAATATGATGACGATGATGTTTACAGAGGCCA 120  
QY 3434 AAGAGTTGAAAACAG-AGCCAGAGTCTGGAGTTAGATGACAGACACTCAACAT 3492  
Db 121 GAAGGTTGATACCAAGAGGAGGCTGGGTTACATCAAGACACTCAACAT 180  
QY 3493 TGGATGCGCATCTCA 3508  
Db 181 TAGACGGGCTCTGCA 196

RESULT 9  
US-08-232-463-14/C  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHRIFFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232.463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935.313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-Fls  
US-08-232-463-14

Query Match 2.0%; Score 79.2; DB 1; Length 7218;  
Best Local Similarity 5.7%; Pred. No. 3.2e-12;  
Matches 24; Conservative 245; Mismatches 153; Indels 0; Gaps 0;  
QY 3073 TTGAGATTAAGAGCAGAGCTGAGAGGCGCATGAGAGAGACTCTCTACATCAGCCAGA 3132





NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-LA 9721  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6942 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-125-077-3

Query Match 1.88; Score 71; DB 2; Length 6942;  
Best Local Similarity 57.9%; Pred. No. 7.1e-10;

Matches 150; Conservative 0; Mismatches 100; Indels 9; Gaps 1;

QY 1636 TGGTGTCAATTAACCTGCCCCAGGAGGTGTCACTGTGCCCCGCTGTGAGCTCTGTCTGATG 1695  
DB 2538 TGAATCTGTATGATGATGCTGTGCGTACACAGACACGCTGTGAGAGGTGTGACAGAG 2597  
QY 1696 GCTATTGTTGGGAGCCCTTGGGGAACGTGGCCAGTAGAGCCCTTGTCAAGCCCTGTCACT 1755  
DB 2598 GCTATTGTTGGGAGCCCTTGGGGAACGTGGCCAGTAGAGCCCTTGTCAAGCCCTGTCACT 2648  
QY 1756 GCAACACAAAGTGGAGCCCTTGTGCTCCGAGACCTGTGACCGCTGTGACAGGAGGTGTC 1815  
DB 2649 GCAATGACAACTGTACTTCTCCATCCCTGGACACTGTGACAGCTTGTGTGGCTCTGTC 2708  
QY 1816 TGAATGATCAACACACAGAGCTGGGGTCCACTGTGACCACTGTGAAGCAAGAGCTACTATG 1875  
DB 2709 TGAATGATCAACACAGAGCTGGGGTCCACTGTGACCACTGTGACCACTGTGACCACTACT 2768  
QY 1876 GGGACCCGTTGGCTCCCA 1894  
DB 2769 GAGATGCAATGATGATGCA 2787

RESULT 12  
US-08-635-137-1

Sequence 1, Application US/08635137  
Patent No. 5824775

GENERAL INFORMATION:

APPLICANT: SWIMMER, CANDACE  
APPLICANT: SHYJAN, ANNE  
APPLICANT: LEONARDO, DAVID  
APPLICANT: ZHANG, YUAN  
APPLICANT: KENNEDY, TIMOTHY  
APPLICANT: SERAFINI, TITO  
APPLICANT: TESSIER-LAVIGNE, MARC  
TITLE OF INVENTION: HUMAN NETRIN-1  
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/635,137  
FILING DATE:

CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: UC93-300-6

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1848 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 34..1845  
US-08-635-137-1

Query Match 1.38; Score 53.6; DB 1; Length 1848;  
Best Local Similarity 52.1%; Pred. No. 3.3e-05;

Matches 147; Conservative 0; Mismatches 129; Indels 6; Gaps 1;

QY 156 GGCAGCGACCCCTGAGCGGGGAGCCGGCGCCCTGGCCATGCGCTGCGCTGGCTG 215  
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QY 216 AGCTGTACT 275  
DB 991 CCTTCCACTACGACCGGCGCCCTGGCAGCGGCGCCACAGCGCCGGAAGCCAGATGGCGTG 1050  
QY 276 GTCTGTGATGCAACGGGAGTCCAGGCAATGATCTTTGACCAAGAACTTCAACAACG 335  
DB 1051 GCTGTAACTGAACCACTGCAATGCGCGGCGCGCTTCAACATGAGCTCTCAACGCTT 1110  
QY 336 ACAGGA-----AATGATTCGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 389  
DB 1111 TCGGGGCGCAGACCGGAGGTGTCTGCTCAAGTGTGCCCAACACCGCGCGCGCAC 1170  
QY 390 TGCAGAGGTGCAAGCAGATTTTACCGACAGAGAAAG 431  
DB 1171 TGCATTACTGCAAGGAGGCTACTACCGGCAATGGCGCAG 1212

RESULT 13  
US-09-136-981-1

Sequence 1, Application US/09136981  
Patent No. 6218526

GENERAL INFORMATION:

APPLICANT: SWIMMER, CANDACE  
APPLICANT: SHYJAN, ANNE  
APPLICANT: LEONARDO, DAVID  
APPLICANT: ZHANG, YUAN  
APPLICANT: KENNEDY, TIMOTHY  
APPLICANT: SERAFINI, TITO  
APPLICANT: TESSIER-LAVIGNE, MARC  
TITLE OF INVENTION: HUMAN NETRIN-1  
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/136,981  
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/635,137  
FILING DATE:







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OM nucleic - nucleic search, using sw model

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10395.317 Million cell updates/sec

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Perfect score: 3989  
Sequence: 1 tgggtctcttattcacag.....ccagataatgtcttattg 3989

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications, NA:\*

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13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2986.2	74.9	5200	US-10-227-738-12	Sequence 12, Appl
2	2986.2	74.9	5200	US-09-756-071B-12	Sequence 12, Appl
3	2972.8	74.5	5175	US-10-171-311-114	Sequence 114, App
4	2956.4	74.1	5156	US-09-466-386A-130	Sequence 130, App
5	2956.4	74.1	5156	US-09-735-705-130	Sequence 130, App
6	2956.4	74.1	5156	US-09-850-716A-130	Sequence 130, App
7	2956.4	74.1	5156	US-09-897-778-130	Sequence 130, App
8	2949.8	73.9	5460	US-10-044-090-558	Sequence 558, App
9	2726	68.3	4316	US-10-227-738-14	Sequence 14, Appl
10	2726	68.3	4316	US-09-756-071B-14	Sequence 14, Appl
11	515.6	12.9	4948	US-10-037-182-15	Sequence 15, Appl
12	515.6	12.9	5306	US-10-037-182-13	Sequence 13, Appl
13	515.6	12.9	7812	US-10-084-817-81	Sequence 81, Appl
14	515.6	12.9	7923	US-10-299-058-11	Sequence 11, Appl
15	515.6	12.9	7923	US-09-864-864-297	Sequence 297, App
16	514.6	12.9	7263	US-10-037-182-19	Sequence 19, Appl
17	514.6	12.9	7554	US-10-037-182-17	Sequence 17, Appl
18	514.6	12.9	8167	US-10-198-846-9785	Sequence 9785, Ap
19	420.8	10.5	613	US-09-998-598-1569	Sequence 1569, Ap

C	20	410.4	10.3	603	10	US-09-879-536-582	Sequence 582, App	
	21	388	9.7	551	10	US-09-879-536-448	Sequence 448, App	
	22	379	9.5	538	9	US-10-060-036-3398	Sequence 3398, App	
	C	23	366.8	9.2	551	9	US-10-076-622-248	Sequence 248, App
	C	24	366.8	9.2	551	9	US-09-551-621-248	Sequence 248, App
	C	25	366.8	9.2	551	10	US-09-604-287A-248	Sequence 248, App
	C	26	366.8	9.2	551	10	US-09-339-338-248	Sequence 248, App
	C	27	366.8	9.2	551	12	US-10-007-805-248	Sequence 248, App
	28	350.2	8.8	5184	10	US-09-845-583-9	Sequence 9, Appl	
	29	332	8.3	458	9	US-10-060-036-8840	Sequence 3840, App	
	30	265.2	6.6	1778	10	US-09-962-832-128	Sequence 128, App	
	C	31	218.8	5.5	262	12	US-10-033-528-1872	Sequence 1872, App
	32	161.2	4.0	188	9	US-10-025-380-696	Sequence 696, App	
	33	161.2	4.0	188	10	US-09-922-217-696	Sequence 696, App	
	34	161.2	4.0	188	10	US-09-833-263-696	Sequence 696, App	
	35	160.6	4.0	221	10	US-09-998-598-2013	Sequence 2013, App	
	36	140.8	3.5	401	9	US-10-025-380-26	Sequence 26, Appl	
	37	140.8	3.5	401	10	US-09-922-217-26	Sequence 26, Appl	
	38	140.8	3.5	401	10	US-09-833-263-26	Sequence 26, Appl	
	39	132.2	3.3	579	9	US-10-084-817-82	Sequence 82, Appl	
	40	109.8	2.8	129	10	US-09-998-598-1920	Sequence 1920, App	
	41	86	2.2	9503	9	US-10-262-670-1	Sequence 1, Appl	
	42	71.4	1.8	4837	10	US-09-764-877-2839	Sequence 2839, App	
	43	71	1.8	9534	9	US-09-954-531-1380	Sequence 1380, App	
	44	70.4	1.8	32250	9	US-09-764-891-9663	Sequence 9663, App	
	45	70	1.8	781	10	US-09-764-877-2838	Sequence 2838, App	

## ALIGNMENTS

RESULT 1  
US-10-227-738-12  
Sequence 12, Application US/10227738  
Publication No. US20030100529A1

GENERAL INFORMATION:  
APPLICANT: Tryggvason, Karl  
Kallunki, Pekka  
Pyke, Charles

TITLE OF INVENTION: Laminin Chains: Diagnostic and  
Therapeutic Use

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff  
STREET: 300 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/227,738  
FILING DATE: 26-Aug-2002  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/800,593  
FILING DATE: 18-FEB-1997  
APPLICATION NUMBER: US 08/317,450  
FILING DATE: 04-OCT-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Chao, Mark  
REGISTRATION NUMBER: 37,293  
REFERENCE/DOCKET NUMBER: 94,778-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-913-0001  
TELEFAX: 312-913-0002  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5200 base pairs

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?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: cDNA
?      FEATURE:
?      NAME/KEY: sig_peptide
?      LOCATION: 118..183
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: 118..3699
?      FEATURE:
?      NAME/KEY: polyA_site
?      LOCATION: 4433
?      FEATURE:
?      NAME/KEY: polyA_site
?      LOCATION: 5195
?      SEQUENCE DESCRIPTION: SEQ ID NO: 12:
?      US-10-227-738-12

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Db	14 AAGGAAAAAGGAAGGACACAGCGGAGCGGAGCGGAGGAGAAACACCAAC--CGAGCGCGCGGGC	71			
OY	159 AGCGACCCCTGCAGCGCGG-----GACCGCGCGCGCGCTGGCGATCGCTGGCGCTGTG	211			
Db	72 AGCGACCCCTGCAGCGGAGACAGACATGAGCGCGCGGACACCGCATGCTGCGCTGTG	131			
OY	212 GCTGAGCTGCTACCTCTGCTTCTGCTCTCTCTGCGGACCGCGGCGACCTCGCGGAG	271			
Db	132 GCTGGGCTGCTGCTCTGCTG	191			
OY	272 GGAATCTGTGATTTCAACGGGAAATCCAGGAAATGCAATCTTTGACAGAACTTCAAA	331			
Db	192 GGAATCTGTGATTTCAATGGGAAATCCAGGAGATGATCTTTGATCGGAACTTCAACAG	251			
OY	332 ACAGACAGGAATGATTCGCGCTGCTCACTGCAATGACAAACATGATGATCACTG	391			
Db	252 ACAAACTGATATGATTCGCGCTGCTCACTGCAATGACAAACATGATGATCACTG	311			
OY	392 CGAGAGGTGCAAGGACGATTTTACCGACAGAGAGAAAGGACCGCTTTTACCGTCAA	451			
Db	312 CGAGAGGTGCAAGATGCTTTTACCGGACAGAGAAAGGAGCGCTTTTACCGTCAA	371			
OY	452 TTGTAACTCTTAAAGTTCTCTTAAGCGCGAATGACAACTCTGAGCGGTGCACTGTAA	511			
Db	372 TTGTAACTCTTAAAGTTCTCTTAAGTTGCTGATGACAACTCTGAGCGGTGCACTGTAA	431			
OY	512 GCCAGGTGTCAGAGAGACAGGTGTGACCGATGCTGCGCGCTTCCACACACTACGA	571			
Db	432 ACCAGGTGTCAGAGAGACAGGTGTGACCGATGCTGCGCGCTTCCACACACTACGA	491			
OY	572 TGTGCGGTGCGCCCAAGACCAAAGGCTGTAAGCTCAAGTGTGATGACCCAGGTGG	631			
Db	492 TGTGCGGTGCGCCCAAGACCAAAGGCTGTAAGCTCAAGTGTGATGACCCAGGTGG	551			
OY	632 CATCTCAGGGGCGGTGACCTCAGGCGCGCTGTGTCAGAGCGGCTGCACTGAGACG	691			
Db	552 CATCTCAGGGGCGGTGACCTCAGGCGCGCGCTGTGTCAGAGCACTGTACTGAGACG	611			
OY	692 CTGTGATAGGTGTGACACAGGTTTCTATCAACTGGATGGGGGAAACCTCAGGCGTAC	751			
Db	612 CTGTGATAGGTGTGACACAGGTTTCTATCTGTGATGGGGGAAACCTCAGGCGTAC	671			
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Db	672 CCAAGTCTTTTGTATGAGGATTCAGCAGCTGCGGAGCTGTGCAAAATGAGTGTCA	731			
OY	812 TAAATATCTCTGCGCTTCAATCAAGTGTGATGCTGGAAGGCTGTCCAAAGAAAGG	871			

Db	732	TAAAGATCACTTACTACTTTTCATCAAGATTTGTATGGCTTGAAGGCTGTCCAAAGAAATGG	791
QY	872	GTCTCTCGCAAGCTCCAGTGGTCAACAGGCCATCGGGATATATTTAGCTACGACAGC	931
Db	792	GTCTCTCGCAAGCTCCATATGGTCAACAGGCCATCAAGATTTGTTTAGCTCAGCCAAAG	851
QY	932	ATCAGACCTGTCTATTTTGTAGCTCTCTCCAAATTTCTTGGGAATCAACAGGTGAGCTA	991
Db	852	ACTAATATCTGTCTATTTTGTGGCTCTCCCAAATTTCTTGGGAATCAACAGGTGAGCTA	911
QY	992	CGGGCAAGACCTATCTTTTGTAGTACCGTGTGATATGGGAGGACAGACACCATCTGGCCA	105
Db	912	TGGGCAAAAGCTGTCTCTTTGACTACCGTGTGACAGAGAGGACAGACACCATCTGGCCA	971
QY	1052	TGACGTGATCCTGGAAGGTGCTGTCTACAGGATCAACAGCTCCCTTGATGCCACTTAGCA	1111
Db	972	TGATGTGATCCTGGAAGGTGCTGTCTACAGGATCAACAGCTCCCTTGATGCCACTTAGCA	1031
QY	1112	GACACTGCCCTTGGGATCACCAGACTTACACATTCAGATTTAAATGAATCCAGAG	1171
Db	1032	GACACTGCCCTTGGGATCACCAGACTTACACATTCAGATTTAAATGAATCCAGAGCA	1091
QY	1172	TAAATGGAGCCCCGAGCTAAGTTACTTTTGAATATGGAGGTACTGCGGAACCTCACAGC	1231
Db	1092	TAAATGGAGCCCCGAGCTAAGTTACTTTTGAATATGGAGGTACTGCGGAATCTCACAGC	1151
QY	1232	CCTGGGATCCGAGCTACTACGAGGAATACAGTACTGGGTACATTTGACAACTGACCTT	1291
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QY	1292	GATTTTCAGCCCCCGCTTTCTGAGCCCCAGCGCCCTGGGTTGAACATGTATGCCC	1351
Db	1212	GATTTTCAGCCCCCGCTGTCTGAGCCCCAGCACCTGGGTTGAACAGTATATGCCC	1271
QY	1352	TGTTGGCTACAAAGGGGCACTCTCGCAGAGATTTGCTTCCCGCTACAAAGAGATTCAGC	1411
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QY	1412	CAGACTGGGACCTTTTGGCACCTGTAAATCCATGTAACTGCCAAAGGGAGGGGCTGTGCA	1471
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QY	1472	TCCAGACACAGAGACTGTACTCAGGGGATGAGAACTTGACATCCCTGAGTGTCTGA	1531
Db	1392	TCCAGACACAGAGACTGTATTCAGGGGATGAGAACTTGACATCTGACATCTGAGTGTCTGA	1448
QY	1532	CTGGCCCCATTTGGTTTCTACAGAGATCCACAGACCCCCCGCAGCTGTGCAAGCCGTGCCCTG	1591
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QY	1592	TCGCAATATGGTTACAGCTGCTCCGTATGCTCTGAGACAGAGAGAGGTGTGCTCAATTACTG	1651
Db	1509	TCATTAAGGGGTTCAGCTGTCTCAGTGATTTCCGGAACAGAGAGAGGTGTGCTCAATTACTG	1568
QY	1652	CCCCCAGGGGTCTCACTGGTCCCGCTGTGACTCTGTGCTGATGAGCTATTTTGGGAGACC	1711
Db	1569	CCCCCAGGGGTCTCACTGGTCCCGCTGTGACTCTGTGCTGATGAGCTATTTTGGGAGACC	1628
QY	1712	CTTGGGGGAACGTGGCCCACTGAGGAGCCCTTGCACCCCTGTACAGTGTGCAACAACTGTGA	1771
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Db	1749	CACAGCGGGATCTACTGTGCGACAGGTCAAAAGAGGCTACTTGTGGGGAGACCATTTGGCTCC	1808
QY	1892	CAATTCAGACAGACAGTGTGAGCTTGCACATGCAACCTCAACAGTGGGCTCGGAGCTGTGGA	1951
Db	1809	CAATTCAGACAGACAGTGTGAGCTTGCACATGTAACCCATGGGCTCAAGAGCTGTGAGG	1868

1952 GTGTGAAGTATGAGCAGCTGTGTTGCAAGCCAGAGCTTGTGGCTCAGCTGTGAGCA 2011  
1869 ATGTGCAAGTATGAGCAGCTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 1928  
2012 TGGCGCAGTGCAGCAGCTGTGAGCTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 2071  
1929 TGGAGCAGTGCAGCAGCTGTGAGCTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 1985  
2072 TATGACAGAGCTGCAGAGTGTGAGAGGCTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 2125  
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2046 AGTACCCAGAGCTGCAGAGTGTGAGAGGCTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 2105  
2186 TGTGAGAGAGCCAGAGTGTGAGAGTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 2245  
2106 TGTGAGAGAGCCAGAGTGTGAGAGTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 2165  
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2366 CACTGAGAGCTGCAGAGTGTGAGAGGCTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 2425  
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3677 AGATGAGTGTGAGAGTGTGAGAGGCTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 3736  
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3666 CTGCTACAGTGTGAGAGTGTGAGAGGCTGTGTTGCAAGCCAGAGTGTGTGGCTCAGCTGTGAGCA 3725  
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RESULT 2  
US-09-736-071B-12  
Sequence 12, Application US/09756071B  
Patent No. US20020052307A1  
GENERAL INFORMATION:  
APPLICANT: Tryggevason, Karl  
Kallunki, Pekka  
Pyke, Charles  
TITLE OF INVENTION: Laminin Chains: Diagnostic Uses  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fay Sharpe Fagan Minnich & McKee  
STREET: 1100 Superior Ave, Suite 700  
CITY: Cleveland  
STATE: Ohio  
COUNTRY: USA



```

1      ZIP: 44114
2
3      COMPUTER READABLE FORM:
4
5      MEDIUM TYPE: floppy disk
6
7      COMPUTER: IBM PC compatible
8
9      OPERATING SYSTEM: PC-DOS/MS-DOS
10     SOFTWARE: PatentIn Release #1.0, Version #1.30
11
12     CURRENT APPLICATION DATA:
13
14     APPLICATION NUMBER: US/09/756,071B
15
16     FILING DATE: 08-Jan-2001
17
18     CLASSIFICATION: <unknown>
19
20     PRIOR APPLICATION DATA:
21
22     APPLICATION NUMBER: US 09/663,147
23
24     FILING DATE: 150-September 2000
25
26     ATTORNEY/AGENT INFORMATION:
27
28     NAME: Minnich, Richard, J
29
30     REGISTRATION NUMBER: 24,175
31
32     REFERENCE/DOCKET NUMBER: TRV 20014
33
34     TELECOMMUNICATION INFORMATION:
35
36     TELEPHONE: 216-861-5582
37
38     TELEFAX: 216-241-1666
39
40     INFORMATION FOR SEQ ID NO: 12:
41
42     SEQUENCE CHARACTERISTICS:
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44     LENGTH: 5200 base pairs
45
46     TYPE: nucleic acid
47
48     STRANDEDNESS: single
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50     TOPOLOGY: linear
51
52     MOLECULE TYPE: cDNA
53
54     FEATURE:
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56     NAME/KEY: sig_peptide
57
58     LOCATION: 118..183
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60     FEATURE:
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62     NAME/KEY: CDS
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64     LOCATION: 118..3699
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66     FEATURE:
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68     NAME/KEY: polyA_site
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79     US-09-756-071B-12

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Query Match	Similarity	88.5%	Pred. No. 0	Mismatches	403	Indels	30	Gaps	7
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Db	72	AGCGACCCCTCAGAGGGAGACAGACATGAGGGGCGCGGACCGGCATCCCTGGCTCTG	131						
QY	212	GCTGAGCTGTACTCTGCTTCTGCTCTCTCTGCGCGCAGCGCGGCGACCTCCGGAG	271						
Db	132	GCTGGGCTGTGCTCTGCTG	191						
QY	272	GGAAGTCTGTATGTTCACAACGGGAAGTCCAGGCATGACATCTTTGACCAAGAACTTCACA	331						
Db	192	GGAAGTCTGTATGTTCACAATGGGAATCCAGGCAAGTATCTTTGATCGGGAATTCACAG	251						
QY	332	ACAGACAGGAANTGGATCCGCTGCGCTCAACATCGCAANTGACAACTGATGGCATCCACG	391						
Db	252	ACAACACTGTATGTATGATTCGCTGCTCTTAACCTGCATATACACACTGATGGCATTCACG	311						
QY	392	CGAGAGGTCAAGGCGAGATTTTTCACGACAGAGAGAAAGGAGCCGCTTTTACCTCGCA	451						
Db	312	CGAGAGGTCAAGGATGCGCTTTTTCACGCGACAGAGAAAGGAGCCGCTTTTCCCTCGCA	371						
QY	452	TTGTACTCTTAAAGTTCTTTAGCGCTGCATGTGACAACCTTGACGCGTGCAGCTGTAA	511						
Db	372	TTGTACTCTTAAAGTTCTTTAGTGTGATGTGACAACCTTGACGCGTGCAGCTGTAA	431						

OY	5112	GCACAGTGTGACAGAGACAGTGTGACACGATGTCGTGGCCGCTTCCACACATCTACGA	571
Db	432	ACCAAGTGTGACAGAGAGCCACATGCGACGATGTCTGTGCAAGCTTCCACATGCTCACGGA	491
OY	5712	TGCTGGGTGCGCCCAAGACCAAGGCTGCTAGACTCCAAAGTGTGACTGTGACCCAGCTGG	631
Db	492	TGCGGGGTGACCCCAAGACCGAGACACTGCTAGACTCCAAAGTGTGACTGTGACCCAGCTGG	551
OY	632	CATCTCAAGGGGCGCTGTGACTGAGCGGCTGTGTGTGCAAGCGGGGCTGTCACTGTGAGAGCG	691
Db	552	CATGCGAGGGCGCTGTGAGCGGGGCGGCTGTGTGTGTGCAAGCGCACTGTACTGTGAGAGCG	611
OY	692	CTGTGATAGTGTGCGACCGGTTACTATACACTGGATGGGGGAAACCCCTCAGGCGCTGTAC	751
Db	612	CTGTGATAGTGTGCGATCAGGTTACTATATCTGGATGGGGGAAACCCCTGAGGCGCTGTAC	671
OY	752	CCAGTGTGTTTTGCTATGAGGCAATTCGCGCAGCTGGCCACAGCTCTGGGGACATCTACATGTGCCA	811
Db	672	CCAGTGTGTTTTGCTATGAGGCAATTCGCGCAGCTGGCCGACGCTCTCAAAATATCAATGTGCCA	731
OY	812	TAAATATCATCTCTCCCTTCATCAAGATGTGTAGTGGCTGGAAAGGCTGTCCAAAGAAACGG	871
Db	732	TAAATATCATCTCTACCTTTTCAATCAAGATGTGTAGTGGCTGGAAAGGCTGTCCACAGAAATGG	791
OY	872	GTCCTCTGCAAAAGCTCCAGTGTGACAGAGCGCCATCGGGATATATTTAGTCTAGCAGCAGCG	931
Db	792	GTCCTCTGCAAAAGCTCCAAATGGTTCACAGCGCCATCAAGATGTGTAGTCTAGCAGCGCAACG	851
OY	932	ATCAGACCCGCTCTATTTTGTAGTGTCTCGCCAAATTTCTTGGGAAATCAACAGGTGACTTA	991
Db	852	ACTAGATCTGTCTATTTTGTGTGTCTCGCCAAATTTCTTGGGAAATCAACAGGTGACTTA	911
OY	992	CGGGCAAAAGCTATCTTTTGTAGCTACCGTGTGTGATAGGGGAGGCGACACCCATCTGGCCA	1051
Db	912	TGGGCAAAAGCTGTCTTTTGTAGCTACCGTGTGTGACAGAGGAGCGACACCCATCTGGCCA	971
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Db	972	TGATGTGATCTGTGGAAGTGTGTGTGTCTACAGGATTCACAGCTCCCTTGATGTGCACCTTGGCAA	1031
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Db	1032	GACACTGCGCTGTGGGCTCACCAAGACTTACACATTTAGGTTAAATGAGATCCACAAACA	1091
OY	1172	TAAATGAGCCCCAGCTAAGTACTTGTAGATGTGAGAGGTTACTGCGAACCCTCAGACG	1231
Db	1092	TAAATGAGCCCCAGCTGAGTACTTGTAGATGTGAGAGGTTACTGCGGATCTCAGACG	1151
OY	1232	CCCTCGGGATCCGACTACCTACGAGAGATACAGTACGAGGATCTGACAAACGTCGACTT	1291
Db	1152	CCCTCGGATCCGACTACATATGGAAGATACAGTACGAGGATCTGACAAATGTGACACT	1211
OY	1292	GATTTCAAGCCCGCCGTTCTGTGAGGCCACAGCGCCCTGGGTTGAAACATGTGTATCCC	1351
Db	1212	GATTTCAAGCCCGCCGCTGTCTGTGAGGCCACAGCCCTGGGTTGAAACAGTGTATGTCC	1271
OY	1352	TGTTGGCTACAAAGGGGAGTCTTCTCCAGAGATGTGTCTCCGGCTACAAAGAGATTTACG	1411
Db	1272	TGTTGGGTACAAAGGGGCAATTTCTCCAGAGATGTGTCTTCTGGCTACAAAGAGAGATTTACG	1331
OY	1412	CAGACTGGGACCTTTTGGCACTGTATTTCAATGTAACTGGCAAGGGGAGGGGCGCTCGCA	1471
Db	1332	GAGACTGGGGCTTTTGGCACTGTATTTCTTGTAACTGTCAAGGGGAGGGGCGCTGTG	1391
OY	1472	TCCAGACACAGAGACTGTATTACTAGGGGATGAGAACCTGTACATCTCCTGATGTGCTGA	1531
Db	1392	TCCAGACACAGAGATGTATTACTAGGGGATGAGAAATCTGACAT--TGATGTGTGCTGA	1448
OY	1532	CTGGCCCATTTGGTTTTCACAAAGATTCACAAAGACCCCGGACGTGCAAGAGCCGTGGCCCTG	1591
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[illegible]

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Db	2706	TCAGTCCCTTACGATGGAGAAGAACAGAGATCAAAACAAAAGCGATTCACCTCTCAAG	2765
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Db	2886	GCTTTCCTCCGTCCCAACTTGTCTAAAGCAGAGCCCAAGAACACTAGTATGGGCAATGC	2945
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Qy	3077	AGATTAAGACACAGAGCTGGAAGAGCCCATAGAGACTCTCTCAATCAGTACACAGAAAGGT	3136
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Db	3066	TTCAGATCCAGTGCACAGAGCAAGCAAGCAGAAAGCAGCCCTGGGCAAGTGCCTGC	3125
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Db	3366	GGTTGATATCCAGAGCCAGAAAGCGCTGGGGTTTACATTCACACACACTCAACATTTGGA	3425
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Db	3606	AGATGGAATTCGGGCTGATGTAAGAACTTGAAGGACATCAAGGAGCACTGGCCCCGGG	3666
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RESULT 3  
US-10-171-311-114  
; Sequence 114, Application US/10171311  
; Publication No. US2003008270A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlegel, Robert  
; APPLICANT: Chen, Yan  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Monahan, John  
; APPLICANT: Kamakar, Shubhangl  
; APPLICANT: Ghatt, Karen  
; APPLICANT: Gannavarapu, Manjula  
; APPLICANT: Hoerish, Sebastian  
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
; TITLE OF INVENTION: OF CERVICAL CANCER  
; FILE REFERENCE: MRI-035  
; CURRENT APPLICATION NUMBER: US/10/171,311  
; CURRENT FILING DATE: 2002-06-12  
; PRIOR APPLICATION NUMBER: US 60/298,159  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,155  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/335,936  
; PRIOR FILING DATE: 2001-11-14  
; NUMBER OF SEQ ID NOS: 238  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 114  
; LENGTH: 5175  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-171-311-114

Query Match 74.5%; Score 2972.8; DB 9; Length 5175;  
Best Local Similarity 88.5%; Pred. No. 0;  
Matches 3314; Conservative 0; Mismatches 402; Indels 30; Gaps 7;

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QY 174 GGGGAGC-----GCGGCGGCGCTGCGATGCTGCGCTGCTGAGCTGCTACCT 226  
Db 59 GGGAGACAGACTGAGCGCGCGCGCGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCT 118  
QY 227 CTGCTTCTGCTCTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 286  
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QY 287 CAACGGAGTCCAGGCAATGATCTTTGACAGGAATTCACAAAAGACAGAGAAATG 346  
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QY 407 AGGATTTTACGACAGAGAAAGGAGCGCTGTTTACCCTGCAATTTGAATCTTAAGG 466  
Db 299 TGGCTTTTACGACAGAGAAAGGAGCGCTGTTTACCCTGCAATTTGAATCTTAAGG 358  
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Db 359 TTCTCTTACGCTCGATGTGACAACTTGAGCGTGCAGCTGTAAACAGAGGTGACAG 418  
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Db 1379 TGTCTTATGAGGAGATGAGAAATCTGACAT---TGAGTGTGCTGACTGCCCCATGTTT 1435  
QY 1547 CTACAAAGATCCAAAGAGCCCGCGAGCTGCAAGCCGCTGCTGCTGCAATGAGTTCA 1606  
Db 1436 CTACAAAGATCCAAAGAGCCCGCGAGCTGCAAGCCGCTGCTGCTGCAATGAGTTCA 1495  
QY 1607 CTGCTCGGTGATGCTGAGACAGAGAGGTGATGCTCAATTAATGCTGCCCGCAGGTTCA 1666

Db	1496	CTGCTCAGTGAATGCCGGACGACGGAGAGGTGTGTCATAATTAAGTCCCTCCCGGGGTAC	1553
OY	1667	TGATGCCCGCTGTAGAGCTGTGTGCTGTAATGGCTATTTTGGGGAGCCCTTCCGGAGAACGTGG	1726
Db	1556	CGATGCCCGCTGTAGAGCTGTGTGCTGTAATGGCTACTTTTGGGGAGCCCTTGTGTGAACATGG	1615
OY	1727	CCCAATGAGGCTTGTAGCCCTGTCTAGTGCATCAACACACGTGGACCTTATGTGCTCCGG	1786
Db	1616	CCCAATGAGGCTTGTAGCCCTGTCTAGTGCATCAACACACGTGGACCTTATGTGCTCCGG	1675
OY	1787	GAATGTGACCCGCTGACAGGACAGGTGTCTGAATGCATCCACAAACACAGTGGGGTCCA	1846
Db	1676	GAATTTGTGTACCCGCTGACAGGACAGGTGTCTGAATGTATCCACAAACACAGCCGCTCACTA	1735
OY	1847	CTGTGACACAGTGCACAAACAGGCTCTACTATGGGGAGCCGCTTGGCTCCCATCCAGAGACAA	1906
Db	1736	CTGTGACACAGTGCACAAACAGGCTCTACTTCCGGGGACCCATTGGCTCCCAACCCAGAGACAA	1795
OY	1907	GTTGTGAGCTTGTCAACTGTCAACCCAGTGGGCTCGGAGCCTGTGAGTGTGTGAATGTATGG	1966
Db	1796	GTTGTGAGCTTGTCAAACTGTCAACCCAGTGGGCTCGGAGCCTGTGAGTGTGTGAATGTATGG	1855
OY	1967	CAGCTGTGTGTGCAAGCCAGGCTTTGGTGGCTTACGTGTGAGCATGCGGCACTGACACG	2026
Db	1856	CACCTGTGTGTGCAAGCCAGGATTTGGTGGCCCACTGTGAGCATGTGAGCATTT--CAG	1912
OY	2027	CTGTCCAGGCTTGCATATATCAAGTGAAGGTTCAATGATGATGATTTTATGGACGACGTCCA	2086
Db	1913	CTGTCCAGGCTTGCATATATCAAGTGAAGATTTCAATGATGATGATTTTATGGACGACGTCCA	1972
OY	2087	GATCCTGAGGAGCCCTGATTTTCGAAGGCTCAAGG-----TGGACAGTATCCCAACGACGA	2140
Db	1973	GAGATATGAGGAGCCCTGATTTTCGAAGGCTCAAGGAGTGTGATGTGAGTATGATCTGATACAGA	2032
OY	2141	GCTGGAAGGACAGATGACAGCAGGCTGTAGCAGGAGCCCTTCCGGACACTTTCAGAGAACCCCA	2200
Db	2033	GCTGGAAGGACAGATGACAGCAGGCTGTAGCAGGAGCCCTTCCAGACACTTTCAGAGATGTGCCA	2092
OY	2201	GATTTCAACAAATGCTGTTAGATCTCTCAATCTCCGGGTGGCCCAAGGCAAGGACATCCAGA	2260
Db	2093	GATTTCAACAAATGCTGTTAGATCTCTCAATCTCCGGGTGGCCCAAGGCAAGGACATCCAGA	2152
OY	2261	GAATAGCTACCGGGAGCCGCTGTGATGTGACCTCAAGATGACCTGTGGAAAGATTTCCGGGCTT	2320
Db	2153	GAACAGCTACCGAGACCGCCCTGTGATGTGACCTCAAGATGACCTGTGGAAAGATTTCCGGGCTT	2212
OY	2321	GGGCAATCAGTATCAGAACCAAGTTACAGATTAATCTGCAAGGCTCACTACTCAGATGCGCT	2380
Db	2213	GGGCAATCAGTATCAGAACCAAGTTCCGGGATATCTACAGGCTCACTACTCAGATGACAGCT	2272
OY	2381	GAGGCTGGAGAAAGTGAAGCTTCCCGTCAAAACCAACAACTTCTCCTTCAGAGCACTA	2440
Db	2273	GAGGCTGGAGAAAGTGAAGCTTCCCGTGGGAAACCACTAACATTTCTGCTTACAGCACTA	2332
OY	2441	CGTGGGGCCAATGGCTTTAAAGTCTGAGCTCAGAGAGGCCACGAGATTTGGCAGACACACCA	2500
Db	2333	CGTGGGGCCAATGGCTTTAAAGTCTGAGCTCAGAGAGGCCACCAAGATTTAGCAGAAAGCCA	2392
OY	2501	TGTTCACTCAGCCACGTAACTATGAGACCACTGGCAAGGAAGGAACCAAGAGATTTCCAAAGA	2560
Db	2393	CGTTAGAGTCAAGCCAGTAACTATGAGAGCAACTGACAAAGGAAGAACTGAGACTTTTCCAAACA	2452
OY	2561	GCTATGTCACTGAGTGGCGCGAGGCTGTGCAAGGAAGAG--GCGGAACCGGCAAGCT	2614
Db	2453	AGCCCTCACTGAGTGGCGCGAGGCTGTGCAAGGAAGGATCGGAAGCGGAACGGGTAGGCC	2512
OY	2615	GGAGGAGACCCCTGTGTGCAAAAGCTTTGTGGAAAAATTTGCAGAAAACTAAATCTTCGGCCA	2674
Db	2513	GGAGGAGTCTGTGTGTGCAAAAGGCTTTGTGTGGAAAAATTTGTGAGAAAAACCAAGTCCCTGGCCA	2572
OY	2675	GGAGTGTGTGAGGAGGAGCCACGCAAAACCCAGCATGGAAGCAGATAGGTTTATTCAGATAG	2734
Db	2573	GCAGTGTGTGAGGAGGAGCCACCTCAAGCGGAATTTGAAGCAATATAGTGTATTCAGACACAG	2632

QY	2735	TTCTCCACCTTCTCAATTCCGTGTCTCAGATTACAGGAGTCAATATCATAGTCTCTTCAGGT	2794
Db	2633	TTCTCCGCTCTCTGGAATCTAGTGTCTCGGCTTCAAGGAGTCTAGTATCATGCTCTCTTCAGGT	2692
QY	2795	-- --GGAACCGAAGAGGGCTCAGACAAAAAGCTGATTCTCTCTCAACCGGTGTGACTTAAGCA	2851
Db	2693	GGAAAGAACAAAGAGAGATCAACACAAAAAGCGATTCTCTCAACGCTGGTATACCAAGCA	2752
QY	2852	TATGGATGAGTTCAAGCACGTGCAAGCAATCTGGGAAACTGGAGAAAGAAACCCGGCA	2911
Db	2753	TATGGATGAGTTCAAGCCTTACACAAAAACAACTGGGAAACTGGAAAGAAAGACACAGCA	2812
QY	2912	GCTCTTACAGAAATGGAAAGATGGGAGACACACATCAGATACGTGCTTCCCTGGCCAA	2971
Db	2813	GCTCTTACAGAAATGGAAAAAGTGGAGAGAAATACAGATACGTGCTTCCCTGGCCAA	2872
QY	2972	CCTTGCTTAAAGCAGAGCCCAAGAAAGCACTAAGTATGGGGCAATGCCACTTTTATGAAGT	3031
Db	2873	TCTTGCTTAAAGCAGAGCACAAAGAAAGCACTAAGTATGGGCATGCCACTTTTATGAAGT	2932
QY	3032	TGAGAACACTTTAAAGATCTCAGAGATTTGACCTGCAAGTTGGAGTAAAGACGCA	3091
Db	2933	TGAGAGCACTCCTTAAAAACCTCAAGAGATTTGACCTGCAAGTGCACAAACAAAAAGCA	2992
QY	3092	AGCTGAAGAGGCCATGGAAGAGACACTCTCATATCAGCCAGAAAGTTGAGGTGGCAGCA	3151
Db	2993	AGCTGAAGAGGCCATGGAAGAGACACTCTCATATCAGCCAGAAAGTTTTCAGTATGCCATGA	3052
QY	3152	CAAGACGAAGCAGACAGAACGACGCCCTGGGACAGTGTCTGCCACGACGCCCAAGAGGCAAA	3211
Db	3053	CAAGACCCAGACAGAGAAAGGCCCTGGGAGAGCGCTCTGATGCACAGAGAGGCAAA	3112
QY	3212	GAATGCACACCGAGGAGGCCCTGGAGATCTCTGGCAAGTTAACAAGAGATAGAGAGTCT	3271
Db	3113	GAATGGGGCCGGGAGGCGCTTGGAATTTCCAGTGAATTAACAGGAGATTTGGAGTCT	3172
QY	3272	GAACTTGGAAACCCATGTGACAGACAGATGAGAGCCTTGGCCATGTGAGAAAGGACATCGGCCAC	3331
Db	3173	GAACTTGGAAACCCATGTGACACGACAGATGAGAGCCTTGGCCATGTGAGAAAGGACATCGGCCCTC	3232
QY	3332	TCTGAAAAAGTGAATGAGAGAAAGTGGAAAGAGAGCTGTCAAGGAAGAGCAGAGATTGGA	3391
Db	3233	TCTGAAAGAGTGAATGAGAGAAAGTGGAAAGAGAGCTGTGAAAGGAAGAGCTGTGGAGTTGGA	3292
QY	3392	CATGAGATTTGGACGACAGTGCAGATGGGTAAATTGACAGAGGCCCAAGAGAGTTGAAACAGAGC	3451
Db	3293	CACGAAATTTGATGCAGTACAGATGGTATTTACAGAAAGCCCAAGAAAGTTGATACCAGAGC	3352
QY	3452	CAAGAATCTGGAAGTTACGATCCAAGACACACTCAACCATTTGGATGGCATCTPACACT	3511
Db	3353	CAAGAACCTGGGGTTTACAATCCAAGACACACTCAACCATTTAGACGGCCTCTCCATCT	3412
QY	3512	AATGAGCAGCGCTGGCAGCTGTGGATGGAAGAGAGTGATCTTACTGGAGCGAAGCTTTT	3571
Db	3413	GATGAGCCAGCGCTCTCACTGTGATGGAAGAGAGGGGTGGTCTTACTGGAGCGAAGCTTTT	3472
QY	3572	CCGAGGCCAAGACTCGATCAACAGCAGCACTACGGCCCTTGATGTGCAGAGCTGGAAGAGAG	3631
Db	3473	CCGAGGCCAAGACCCGATCAACAGCAGCACTCGGGCCCATGTATGTCCAGAGCTGGAAGAGAG	3532
QY	3632	GGCACATGGCAGAAAGGCCACATCTCGTTTCTCTGAGACTAGCATAGTGGGATTTCTGGC	3691
Db	3533	GGCAGCTGAGAGAGAGGGCCACATCTCATTTCTGTGGAGCAAGACATAGATGGGATTTCTGGC	3592
QY	3692	TGATGTGAAGAACTCGGAGAACATCAGGGAACACTGGCCCCGGGCTCTCAATATACCA	3751
Db	3593	TGATGTGAAGAACTTGGAGAACTTAGGAGACAACCTGGCCCCAGGCTCTCAATATACCA	3652
QY	3752	GGCTCTTGAGCAACAGTAGAGCTGCTTGAAGATTTCTCAACCAAGTTCTTGGATTTCA	3811
Db	3653	GGCTCTTGAGCAACAGTAGAGCTGCTCAATTAATTTCTCAACTGAGGTTCTTGGATTTCA	3712



Db 1744 ACCATTGGCTCCCAACCCAGACAAAGTGTGAGCTTGCACACTGTAAACCCCATGGGCT 1803  
Oy 1939 CGAGACCTGTGAGTGTGAAGTATGGCAGCTGTGTTTGCAGCCAGGCTTTGTGGCC 1998  
Db 1804 CAGAGCCTGTAGATGTGAGATGTATGGACCTGTGTGTAACCCAGATTTGTGGCC 1863  
Oy 1999 TCAGCTGTGACATGTGAGCAGCTGACAGCTGTGCCAGCTGTATATATCAATGTAAGTTC 2058  
Db 1864 CCAACTGTGACATGTGAGCACTT---CAGCTGTCCAGCTGTGTATATCAATGTAAGTTC 1920  
Oy 2059 AGATGATCACTTTATGACAGCAGCTCCAGATCTGAGAGCCCTGATTTGAGAGCTCAGG 2118  
Db 1921 AGATGATCACTTTATGACAGCAGCTTCCAGATATGAGAGCCCTGATTTCAAGAGCTCAGG 1980  
Oy 2119 G-----TGAGAGTATCCCAACGAGAGCTGGAAGGAGGATGAGAGCTGAGAGCTGAGAGG 2172  
Db 1981 GTGGTGTGATGATGTATGATCTGTATACAGCTGTGAGAGGAGGATGAGAGCTGAGAGGAGG 2040  
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Db 2041 CCCTTCCAGACATTTCTGAGAGATGCCAGATTTTCAAGAGGATGATCCCTTGTGTC 2100  
Oy 2233 TCCGGGTGGCCAGAGCAGAGCTCAAGAGATACCTACCGGAGCCGCTGGATGATCTCA 2292  
Db 2101 TCCAGTTGGCCAGAGTGTGAGGAGCCAGAGACCTACAGAGCCGCTGGATGATGATCTCA 2160  
Oy 2293 AGATGATCTGTGAGAGAGTGTGGGCGCCGTGGGAGCTGATGATGAGAGCCAGATTTGAGAGTA 2352  
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Oy 2353 CTCGAGGCTGATCACTGATGATGCGCTGAGCTGTGAGAGAGTGAAGCTTCCCTGCATA 2412  
Db 2221 CTCAGAGCTGATCACTGATGATGAGCTGAGCTGTGAGAGAGTGAAGCTTCCCTGGGATA 2280  
Oy 2413 ACACCAACATCTCTCTCTCAAGACATACGTGGGGCCCAATGCTTTAAAGTCTGGCTC 2472  
Db 2281 ACCTTAACATCTCTCTCTCAAGACATACGTGGGGCCCAATGCTTTAAAGTCTGGCTC 2340  
Oy 2473 AGGAGGCCAGAGATTTGACAGAGCCATGTTGATGAGCCAGTAACTGAGAGCAACTGG 2532  
Db 2341 AGGAGGCCAGAGATTTGACAGAGCCATGTTGATGAGCCAGTAACTGAGAGCAACTGGA 2400  
Oy 2533 CAAGAGAAACCCAGAGATTTTCAAGAGCTGATGATCACTGGTGGCGAGAGCTGTGCAGG 2592  
Db 2401 CAAGAGAAACCCAGAGATTTTCAAGAGCTGATGATCACTGGTGGCGAGAGCTGTGCAGG 2460  
Oy 2593 AAGAG-----GGGAGAGCCGAGAGCTGTGAGAGCCGCTGTGTAAGGCTGTGGGATA 2646  
Db 2461 AAGGAGTGTGAGAGCCGAGAGCTGTGAGAGCCGCTGTGTAAGGCTGTGGGATA 2520  
Oy 2647 AATTGCAAGAAACCTAATCTCTGTGAGCCAGAGTGTGTCGAGGAGAGCCACAGCAACGACA 2706  
Db 2521 AATTGCAAGAAACCTAATCTCTGTGAGCCAGAGTGTGTCGAGGAGAGCCACCTCAAGCGGAAA 2580  
Oy 2707 TGAAGCAGATAGTCTTATGACAGATGTCTCAACTTCCGTGCTCAGATTC 2766  
Db 2581 TGAAGCAGATAGTCTTATGACAGATGTCTCCGCTCTGATTCAGTCTGTGCGGCTTC 2640  
Oy 2767 AGGAGTCAATGATAGTCTTGAAGGT---AGAGCAAGAGAGCTGAGAGCAAGAAAGCTG 2823  
Db 2641 AGGAGTCAATGATAGTCTTGAAGGTGAGAGCAAGAGAGTGAAGCAAGAAAGAGG 2700  
Oy 2824 AATTCTCTCAACCGTGTGACTAAGCATATGATGATGATGATGATGATGATGATGATGATGATG 2883  
Db 2701 AATTCTCTCAACCGTGTGATACAGGCAATGATGATGATGATGATGATGATGATGATGATGATG 2760  
Oy 2884 TGGGAACCTGGAGAGAGAAACCCGAGCTTTACAGAAATGAGAAAGATGGAGACACAGA 2943  
Db 2761 TGGGAACCTGGAGAGAGAAACCCAGAGCTTTACAGAAATGAGAAAGATGGAGAGAGA 2820  
Oy 2944 CATCAGATCAGCTGCTTCCGCTGCAACCTGTGTAAGAGAGAGAGCCCAAGAGACTTAA 3003  
Db 2821 AATTCAGATCAGCTGCTTCCGCTGCAACCTGTGTAAGAGAGAGAGCCCAAGAGACTTGA 2880

Oy 3004 GTATGGCAATGCCACTTTTATGAGTGTGAGAACATCTTAAAGATCTCAGAGATTTG 3063  
Db 2881 GTATGGCAATGCCACTTTTATGAGTGTGAGAACATCTTAAAGATCTCAGAGATTTG 2940  
Oy 3064 ACCTGACAGTTGAGATTAAG 3123  
Db 2941 ACCTGACAGTTGAGATTAAG 3000  
Oy 3124 TCAGCAGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAG 3183  
Db 3001 TCAGCAGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAG 3060  
Oy 3184 GTGCTGCTGCCAG 3243  
Db 3061 GCGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3120  
Oy 3244 GCAAGATAGAAACAGAGATAGAGAGTGTGAACCTTGAAGCCATGTGACAGAGATGAG 3303  
Db 3121 GTGAGATTAAGAGAGATTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAGAGTTGAG 3180  
Oy 3304 CCTTGGCCATGAG 3363  
Db 3181 CCTTGGCCATGAG 3240  
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Oy 3424 CAGAGGCCCAAG 3483  
Db 3301 CAGAGGCCCAAG 3360  
Oy 3484 TCAGACATTTGAG 3543  
Db 3361 TCAGACATTTGAG 3420  
Oy 3544 GCGTATCTTACTGTGAG 3603  
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Oy 3604 GCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3663  
Db 3481 GCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3540  
Oy 3664 TGAAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3723  
Db 3541 TGAAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3600  
Oy 3724 ACCTGCCCCCGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3783  
Db 3601 ACCTGCCCCCGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 3660  
Oy 3784 AATTCTCAACCAAGTTCTTGGATTCAGAGCTGATGATGATGATGATGATGATGATGATG 3837  
Db 3661 AATTCTCAACCAAGTTCTTGGATTCAGAGCTGATGATGATGATGATGATGATGATGATG 3714

RESULT 5  
US-09-735-705-130  
; Sequence 130, Application US/09735705  
; Patent No. US20020052329A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skelky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.





QY	2059	AGATGAGTACATTTATGAGCAGGCTCCAGATCCGAGGAGGCCGCTGATTTCCAGAGGCTCAGG	2110
Db	1921	AGATGATCACTTTATGACGACGCTTCCAGAAATGAGGCGCCCTGATTTCAAAGGCTTCAGG	1980
QY	2119	G-----TGAGACAGTACCCACACGACAGCTGGAAGGCAGGATGACAGCTGAGCAGG	2172
Db	1981	GTGGTGAATGAGTATGATACAGAGCTGGAAGGCAGGATACAGCAGGCTGAGCAGG	2040
QY	2173	CCCTTCGGGACATTTCTGAGAGAAACCCAGATTTTCACAAGATGCTGTTAGATCCTTCAATC	2232
Db	2041	CCCTTCAGGAAATTTCTAGAGATGATCCAGATTTTCAGAAAGGTGCTAGCAGATACCTTGTC	2100
QY	2233	TCCGCGTGCCCAAGCAGCACTCAAGAAATATCTACCGGAGACCGCTGATGATACCTCA	2292
Db	2101	TCCAGTTGGCCAAAGTGAAGGCCAAGAGAAACACTACAGAGCGCGCTGGATGACCTCA	2160
QY	2293	AGATGACTGTGGAAGAAGTTCCGGCCCTGGGCACTCACTATCAGAACCAAGTTCCAGATA	2352
Db	2161	AGATGACTGTGGAAGAAGTTCCGGCCCTGGGCAAGTCACTACAGAACCGATGTTCCGATTA	2220
QY	2353	CTCCAGGCTCATACACAGATGGCGCTGAGCCCTGGAGAAAGTGAAGGCTTCCCTGCAAA	2412
Db	2221	CTCAGAGGCTCATACTACAGATGAGTCACTGAGCTGAGCCTGGCAGAAAGTGAAGCTTCTTGGAAA	2280
QY	2413	ACACCAACATTTCTCTCTCAGAGCAGTACGTGGGGCCAAATGGCTTTTAAAGTCTGGCTC	2472
Db	2281	ACACTAACATTTCTGCTCAGACACCACTACGTTGGGGCCAAATGGCTTTTAAAGTCTGGCTC	2340
QY	2473	AGAGAGCCACAGATTTGGCAGACAGCCATGTTCACTAGTACAGCAGTAACTAGTACAGTAC	2532
Db	2341	AGGAGGCCACAAAGATTGACAGAAAAGCCACGTTGAGTACAGCCAGTAACTAGTACAGTAC	2400
QY	2533	CAAGAGAAACCCAGAGATATTCCAAAGAGCTGATCACTGCTCCGAGAGGCTCTCGAGG	2592
Db	2401	CAAGGAAACCTGAGAGACTATTCCAAACAAAGCCCTCACTAGTGTGCGAAGGCCCTGCATG	2460
QY	2593	AAGAG-----GGGAAAGCGGACGCTGCAAGCAGCCGTGTGCTCAAAAGGCTTGTGGAA	2646
Db	2461	AAGAGTCTGGAAGGGGAAAGCGGTAGCCCGGACGGTGTGTGCTCAAGAGGCTTGTGGAAA	2520
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Db	2521	AATTGGAAGAAACCAAGTCCCTGGCCACAGCATTTGACAAAGGAGGCCATCTCAAGCGAAA	2580
QY	2707	TGGAAGCAGATAGTCTTATCAGCATAGTCTCCACCTTCTCAATTCGCTGCTCAGATTC	2766
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QY	2884	TGGGAATCTGGGAAGAGAGAAACCCGGCAGCTTTACAGATGAGAAAGATGGAGACAGA	2943
Db	2761	TGGGAATCTGGGAAGAGAGAAACCCAGCGCTTTACAGAAATGGAAGAAAGTGGGAGAGAGA	2820
QY	2944	CATCAGATCAGCTGTTTCCCGTGCACCACTTGTGTAAAGCAGAGGCCAAGAACACTTAA	3003
Db	2821	AATCAGATCAGCTGTTTCCCGTGCCTTCTTGTCTTAAAGCAGAGGCCAAGAACACTTGA	2880
QY	3004	GTATGGCAATGCACTTTTATGAAGTTGAAACATCTTAAAGATCTCAGAGAGTTTG	3063
Db	2881	GTATGGCAATGCACTTTTATGAAGTTGAGACATCTTAAAGATCTCAGAGAGTTTG	2940
QY	3064	ACCTGCAAGTGTGAGATTAAGAGACAGAAAGCTGAAAGAGCCATGAAGAGACTCTCTCA	3123
Db	2941	ACCTGCAAGTGTGAGATTAAGAGAACAGAAAGCTGAAAGAGCCATGAAGAGACTCTCTCA	3000

QY	3124	TCAGCCAGAAAGTTGGCAGAGTCCGATGTCACAGACGAGACGACGAAAGCACCCTGGGCA	3183
Dd	3001	TCAGCCAGAAAGTTTCCAGATGCCAGTGCACAGACCACGACAGCAAGCAAGACCCCTGGGGA	3060
QY	3184	GTGCTGCTGCCGAGCCCGAGAGGGCCAAAGAAATGCAGCCAGCCAGGAGGCCCTTGAGATCTCTG	3243
Dd	3061	GGCGTGCCTGATATGCACATGAGAGGGCCAAAGAAATGGGGCCGGGAGAGCCCTTGAAATCTTCCA	3120
QY	3244	GCAGATATGAAACAGAGAGATTGGAGGTCTGAACTTGGAAAGCCATATGCACAGCAATGTGGAG	3303
Dd	3121	GTGAGATTGAACAGAGAGATTGGAGGTCTGAACTTGGAAAGCCATATGTGCACACAGATGGAG	3180
QY	3304	CCTTGGCCATGGAGAAAGGAGCTGGCCACTCTGAAAGAGTGAAGATGAGAAAGTGGAAAGAG	3363
Dd	3181	CCTTGGCCATGGAGAAAGGAGCTGGCCCTCTGAAAGAGTGAAGATGAGAAAGTGGAAAGAG	3240
QY	3364	AGCTGTCAAGAAAGAGAGAGATTTGACATGGATATTTGGACGAGTGCAGATGGTAATT	3423
Dd	3241	AGCTGTCAAGAAAGAGAGAGTGGATTTGACAGAAATATGAGATGCAAGTACAGATGGTGTATT	3300
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QY	3544	GGCTGATATTACTGGAGCAGAAAGCTTTCCAGAGCAACATCTCAGATCAACAGCCAGCTAC	3603
Dd	3421	GGCTGATTTACTGGAGCAGAAAGCTTTCCAGAGCCAAAGCACAATCATCAAGCCACACTGC	3480
QY	3604	GGCCCTTGATGTCAGAGCTGGAAGAGAGGGCACAATCGGCAGAGAGGCCACTCCGTTTCC	3663
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QY	3724	ACCTGCCCCCGGGCTGTACAAATACCAAGGCTCTTGAGACAACAGTGAAGCTTGCCTTAGAG	3783
Dd	3601	ACCTGCCCCCGGGCTGTACAAATACCCAGGCTCTTGAGACAACAGTGAAGCTTGCCTTAAT	3660
QY	3784	ATTTCACAAAGGTTCTTGGAGTACAGACTAGCTGCCTTAAAGATTTCMA	3837
Dd	3661	ATTTCACACTGAGGTTCTTGGAGTACAGATCTCAGGGCTGGGAGGCATGTCA	3714

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      RESULT 6
US-09-850-716A-130
; Sequence 130. Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 130
; LENGTH: 5156
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-850-716A-130

Query Match      74.1%; Score 2956.4; DB 10; Length 5156;
Best Local Similarity 88.4%; Pred. No. 0;
Matches 3285; Conservative 0; Mismatches 401; Indels 28; Gaps 6;
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Db 2161 AGATGACGTGGAAAGGATTGCGGCTCGGGAACTGACGACCAAGCGATTGGGATA 2220  
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Db 2221 CTCACAGGCTCATACATGCGGCTGAGCCGCGGAGAAAGAGAGCTCCCTGCGAA 2280  
Qy 2413 ACACCAACATCTCTCTGAGAGCATGCGGCGCAAAATGCGTTTAAAGTCTGCGTC 2472  
Db 2281 ACATTAACATCTCTCTGAGAGCATGCGGCGCAAAATGCGTTTAAAGTCTGCGTC 2340  
Qy 2473 AGAGGCGCAGAGATTGGCAGACAGCATGTTCACTGACGCCAGTAACTGAGAGCACTGG 2532  
Db 2341 AGGAGCGCAGAGATTGGCAGACAGCATGTTCACTGAGCCAGTAACTGAGAGCACTGA 2400  
Qy 2533 CAAAGGAACCCAGAGATTTCCAAAGAGCATGATGTCAGTCCGCGGAGAGGCTCTGCAGG 2592  
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Db 2461 AAGGAGTCGGAAGGGAAGCGCGTGGTGGAGCGCGTGGTGGTGGTGGTGGTGGTGGTGG 2520  
Qy 2647 AATTGCAAAAACCTAAATCTCTGCGCCAGAGATTGTCGAGGAGGCGCAACGCAACGACA 2706  
Db 2521 AATTGCAAAAACCTAAATCTCTGCGCCAGAGATTGTCGAGAGGAGGCGCAACGCAACGAAA 2580  
Qy 2707 TGGAGAGAGATAGGCTTTATCAGATAGTCTCCACCTTCTCAATCCGCTGCTCATAGATC 2766  
Db 2581 TTGAGAGAGATAGGCTTTATCAGATAGTCTCCACCTTCTCAATCCGCTGCTCATAGATC 2640  
Qy 2767 AGGAGTCAATGATCAGTCTCTGCAAGT---AGAAGGAGAGAGCTGACAGCAAAAGCTG 2823  
Db 2641 AGGAGTCAATGATCAGTCTCTGCAAGT---AGAAGGAGAGAGCTGACAGCAAAAGCTG 2700  
Qy 2824 ATTCTCTCTCAACCGTGTGACTAAGATATGATGATGATGATGATGATGATGATGATG 2883  
Db 2701 ATTCTCTCTCAACCGTGTGACTAAGATATGATGATGATGATGATGATGATGATGATG 2760  
Qy 2884 TGGGAACCTGGGAGAGAGAAACCGGCGAGCTTTACAGAAATGAGAAAGATGGGAGACGA 2943  
Db 2761 TGGGAACCTGGGAGAGAGAAACCGGCGAGCTTTACAGAAATGAGAAAGATGGGAGACGA 2820  
Qy 2944 CATGAGATCAGCTCTTCCCGTCCCAACCTTGTAAAGAGAGAGCCCAAGACACACTAA 3003  
Db 2821 AATGAGATCAGCTCTTCCCGTCCCAACCTTGTGTAAAGAGAGAGCCCAAGACACACTGA 2880  
Qy 3004 GTATGGCAATGCCACTTTTATGAAATGAAATCTTAAAGATCTTCAGAGATTGG 3063  
Db 2881 GTATGGCAATGCCACTTTTATGAAATGAAATCTTAAAGATCTTCAGAGATTGG 2940  
Qy 3064 ACCTCGAGGTGGAGATTAAGAGACAGAGAGCTGAAAGAGCCATGAGAGATCTCTTACA 3123  
Db 2941 ACCTCGAGGTGGAGATTAAGAGACAGAGAGCTGAAAGAGCCATGAGAGATCTCTTACA 3000  
Qy 3124 TCAGCCAGAAAGTTGGAGGTGCCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3183  
Db 3001 TCAGCCAGAAAGTTGGAGGTGCCAGTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060  
Qy 3184 GTGCTGTGCTGCGAGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3243  
Db 3061 GCGCTGTGCTGCGAGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3120  
Qy 3244 GCAGATGAG 3303  
Db 3121 GTGAGATTGAG 3180  
Qy 3304 CCTTGGCCATGAG 3363  
Db 3181 CCTTGGCCATGAG 3240  
Qy 3364 AGCTGTCAAG 3423  
Db 3423 AGCTGTCAAG

Db 3241 AGCTGTCAAG 3300  
Qy 3424 CAGAGCGCCCAAAAGATTGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3483  
Db 3301 CAGAGCGCCCAAAAGATTGAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360  
Qy 3484 TCACACATTTGATGAG 3543  
Db 3361 TCACACATTTGATGAG 3420  
Qy 3544 GCGTGTCTTACTGAG 3603  
Db 3421 GCGTGTCTTACTGAG 3480  
Qy 3604 GCGCTGTGATGATGAG 3663  
Db 3481 GCGCTGTGATGATGAG 3540  
Qy 3664 TGGAGACTAGATGATGAG 3723  
Db 3541 TGGAGACTAGATGATGAG 3600  
Qy 3724 ACTGCCCCCGGCGCTGCTTACATATCCAGAGCTCTTGGAGCAAGTGAAGTCTGAGAG 3783  
Db 3601 ACTGCCCCCGGCGCTGCTTACATATCCAGAGCTCTTGGAGCAAGTGAAGTCTGAGAGAG 3660  
Qy 3784 ATTCTCAACCAAGTCTTGGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3837  
Db 3661 ATTCTCAACCAAGTCTTGGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3714

## RESULT 7

US-09-897-778-130  
; Sequence 130; Application US/09897778  
; Patent No. US20020147143A1

; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
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; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.

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; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778

; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 130

; LENGTH: 5156  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-09-897-778-130

Query Match 74.1%; Score 2956.4; DB 10; Length 5156;  
Best Local Similarity 88.4%; Pred. No. 0;  
Matches 3285; Conservative 0; Mismatches 401; Indels 28; Gaps 6;

Qy 146 CGAGGCGCGGCGAG 198  
Db 7 CGAGGCGCGGCGAG 66  
Qy 199 TGCGTGGCTCTGAG 258  
Db 67 TGCGTGGCTCTGAG 126  
Qy 259 CCACCTCGGAG 318  
Db 127 CCACCTCGGAG 186

QY	319	AGGAACTTCACAAACAGACAGAGAAATGATTCGCCGTGCTTAACCTGCAATGACAACTG	378
Db	187	GGGAACCTTCACAGAAACCTGGTAATGATTCGCCGTGCTTAACCTGCAATGACAACTG	246
QY	379	ATGCACTCAGTGGCAGAGGTGCAAGAGCAGGATTTTACCGACAGAGAAAGGACCGCT	438
Db	247	ATGGCATTCAGTGGCAGAGAGTGCAGAAATGGCTTTTACCGGACACAGAAAGGACCGCT	306
QY	439	GTTTACCTGCATTTGTAATCTTAAGSTCTCTTAAAGCTCTTAAAGCTGATGTGACACTCTGAC	498
Db	307	GTTTGGCCCTGCATTTGTAATCTTAAGSTCTCTTAAAGCTGATGTGACAACTCCGGAC	366
QY	499	GGTGAGCTGAAGCCAGTGTGACAGAGACAGGTGTGACCGAATGTGCCGGGCTTC	558
Db	367	GGTGAGCTGAAGCCAGTGTGACAGAGACAGATGTGACCGAATGTGTGCAAGCTTC	426
QY	559	ACACACTCAGTATGCTGGGTGGCGCCCAAGACCAAGGCTCTAGACTCCAAAGTGTGACT	618
Db	427	ACATGCTCAGGATGTGGGGGTGCACACCACAGACAGACTCTAGACTCCAAAGTGTGACT	486
QY	619	GTCACCCAGCTGGGATCTCAGGGCCCTGTGACTAGCGCCGTGTGTCTGCAAGCCGCTG	678
Db	487	GTCACCCAGCTGGGATCTCAGGGCCCTGTGACTAGCGGGCCGTGTGTCTGCAAGCCAGCTG	546
QY	679	TCACTGAGAGACGGTGTGATAGGTGTGCACACAGGTTACTATACCTGGATGGGAAAC	738
Db	547	TCACTGAGAGAACGGTGTGATAGGTGTGATCAGGTTACTATATCTGGATGGGGAAC	606
QY	739	CTCAGGGCTGTACCACTAGTTTTTTTGTCTATGGGCATTTCCGCCAGCTGCCACAGCTCTGGG	798
Db	607	CTGAGGGCTGTACCCAGTGTCTGTCTATGGGCATTTACGCCAGCTGCCAGCTCTGAC	666
QY	799	ACTACAGTGTCCATTAATCATCTCTGCTTCATCAAGATGTTGATGGCTGGAAAGCTG	858
Db	667	ATATCAGTGTCCATTAAGTATCATCTCTTACTTTCATCAAGATGTTGATGGCTGGAAAGCTG	726
QY	859	TCCAAGAAACGGGCTCTCTGCAAAAGCTCCAGTGTGTCACAGCGCCATCGGATATATTTA	918
Db	727	TCCAAGAAATGGGCTCTCTGCAAAAGCTCCAGTGTGTCACAGCGCCATCAMAATGTGTTTA	786
QY	919	GCTGAGCAGAGCATCAGACCCCTGTCTTTTGTAGCTCCGCGCAAAATTTCTTGGGAATC	978
Db	787	GCTGAGCCCAACGACTAGACCCCTGTCTTTTGTGTGCTCTGCGCAAAATTTCTTGGGAATC	846
QY	979	AACAGGTAGCTAGCGGGCAAGCCTATCTTTTGACTACACGTGTGATAGGGAGGACAGAC	1038
Db	847	AACAGGTAGCTATGCTCAAAAGCCTGTCTTTGACTACCGTGTGACAGAGGAGGACAGAC	906
QY	1039	ACCATCTGCCATGACGTGATCTCTGGAAGGTGCTGCTACGGATCACACACTCCCTTGA	1098
Db	907	ACCATCTGCCATGATGATGATCTCTGGAAGGTGCTGCTACGGATCACACACTCCCTTGA	966
QY	1099	TGCCACTTAGCAAGCATCTGCCCTGTGGGATCACCACAGACTTACACATTCAGATTAATG	1158
Db	967	TGCCACTTGGCAAGCACTGCTGCTGTGGGCTCACCAAGACTTACACANTTCAGGTTAATG	1026
QY	1159	AACATCCAGACGATATTGAGAGCCCAAGCTTAAGTTACTTTGAGTATCGAGGTTACTGC	1218
Db	1027	AGCATTCCAAGAAATTAATTGGAGCCCAAGCTTAAGTTACTTTGAGTATCGAAGGTTACTGC	1086
QY	1219	GGAACCTCAGACCCCTGGCGAATCCGAGTACTTACGGGATTAACAGTATCGGATACANTG	1278
Db	1087	GGAATCTCAGACCCCTGGCATCCGAGCTTAATTAAGGAATTAACAGTATCGGATACANTG	1146
QY	1279	ACAACGTCACCTGATTTTACAGCCGCCCTGTTTGGAGCCCAAGCGCCGGGTTGAC	1338
Db	1147	ACAATGTGACCTGATTTTACAGCCGCCCTGTCTCTGGAGCCCAAGCAACCTGGGTTGAC	1206
QY	1339	AATGTGATGCTCTGTTGGCTTACAAAGGGGCAAGTTCTGCAAGATTTGTCTCGGCTACA	1398
Db	1207	AGTATATATCTCTGTTGGCTTACAAAGGGGCAATTTCTGCAAGATTTGTCTCTGCTTACA	1266

QY	1399	AAAGGATTCACCGAGACTGGGACCTTTGGCACTGTATTCACATGTAACGTCGAAGGG	1458
Db	1267	AGAGGATTCACCGAGACTGGGACCTTTGGCACTGTATTCACATGTAACGTCGAAGGG	1326
QY	1459	GAGGAGCCCTGGGATTCACACACAGAGAGCTTTACTAGGGGATGAGAACCTGACATCC	1518
Db	1327	GAGGAGCCCTGTGATTCACACACAGAGAGTTGTTATTCAGGGGATGAGAACCTGACAT	1384
QY	1519	CTGAGTGTGTACTGCCCATTTGGTTTCTACACAGATCCACAGACCCCGACGTCA	1578
Db	1385	-TGAGTGTGTACTGCCCATTTGGTTTCTACACAGATCCCGACAGACCCCGACGTCA	1443
QY	1579	AGCGTGGCCCTGTGCGCAATGGGTTTACACTGCTCCGTGATATCCCTGAGACACAGAGGTGG	1638
Db	1444	AGCCATGTCCCTGTGCTATACAGGGTTTACACTGCTCTAGTATATCCCGAGACGGAGAGGTGG	1503
QY	1639	TGTGCATTAATGCCCCCAGGAGGTGTCATGTGTGCCCGCTGTGAGCTCTGTCTATGGCT	1698
Db	1504	TGTGCATTAATGCCCCCTCCCGGGGTACACGGGTGCCCGCTGTGAGCTCTGTGTCTATGGCT	1563
QY	1699	ATTTTGGGGACCCCTTCGGGGAGCGTGCGCCAGTGAGGCTTTGTACGCTCTGTCAGTGCA	1758
Db	1584	ACTTTGGGGACCCCTTTGTGTAACATGAGCCAGTGAGGCTTTGTACGCTCTGTCAATGTCA	1623
QY	1759	ACAACACGTGGACCTTAGTGCCTTCGGGAAGTGTGACCCGCTGACAGAGCGTGTCTGA	1818
Db	1624	ACAACAAATGTGGACCCCGAGTGCCTTCGGGAATTTGTACCCGCTTACAGAGCGTGTGTGA	1683
QY	1819	AGTGATCTCACACACACAGCTGGGGTCCACTGTGACACAGTGTGCAAAAGCAGAGCTACTATGGGG	1878
Db	1684	AGTGATCTCACACACACAGCCGGCATCTACTGCGACAGTGTGCAAAAGCAGAGCTACTTGGGG	1743
QY	1879	ACCCTGTGGCTCCCAATCCACAGACAGAAAGTGTGAGCTTGTCACTGCAACCCAGTGGCT	1938
Db	1744	ACCCTGTGGCTCCCAACCCACAGACAGAAAGTGTGAGCTTGTCACTGTAACCCAGTGGCT	1803
QY	1939	CGGAGCCTGTGGAGTGTGGAAGTGTGAGCTGTGTTTGGCAAGCCAGAGCTTTGGTGGC	1998
Db	1804	CAGAGCCCTGTGAGAGTGTGGAAGTGTGGACACTGTGTTTGGCAACCCAGATTTGGTGGC	1863
QY	1999	TCAGTGTGACATATGCGGCACTGTGACACAGCTTCCAGCTTGTATTAATCAATGGAAGTTC	2058
Db	1864	CCAACTGTGACATATGAGCAATT---CACTGTCCAGCTTGTATTAATCAATGGAAGTTC	1920
QY	2059	AGATGATCAGTTTATGACAGCAGCTCCAGATCTGGAGGCCCTGATTTGGAAGCTCAGG	2118
Db	1921	AGATGATCAGTTTATGACAGCAGCTTCAGAAATGAGAGCCCTGATTTCAAGGCTCAGG	1980
QY	2119	G-----TGGAGCAGTACCACAGCAGAGCTGTGGAAGGAGAGATGACAGGCTGACAGG	2172
Db	1981	GTGTGTGATGAGTGTGTACTGTATACAGAGCTGTGGAAGGAGAGATGACAGGCTGACAGG	2040
QY	2173	CCCTTCGGGCAATTCGTGAGAGGCCCGAGTTTACAAAGATGTGTTTGATGCTCTTCAATC	2232
Db	2041	CCCTTCAGCAATTCGTGAGAGTCCCGAGATTTTCAGAGGTGTCTAAGCAGATCCCTTGGTCC	2100
QY	2233	TCCGGGTGGCCCAAGCAGGACTCAAGAGAAATAGCTTACCGGAGCCGCTGGATGACCTCA	2292
Db	2101	TCCAGTGTGCCAAGGTGAGGAGCCAAAGAAACAGGTATACACAAGCCGCTGGATGACCTCA	2166
QY	2293	AGATGACTGTGAAAGAGTTGGGGCCCTGGGCACTCACTATTCAGAACCAAGTTACAGATA	2352
Db	2161	AGATGACTGTGAAAGAGTTGGGGCTTGGGAAGTCACTATTCACAACCAAGTTTGGGATA	2220
QY	2353	CTCGCAGGCTATCACTCAGATGCGGCTGTGAGCTGTGAGGAAAGTGAAGCTTCCCTGCAAA	2412
Db	2221	CTCACAGGCTATCACTCAGATGACGTGAGCCTGGCGAAGAAAGTGAAGCTTCCCTTGGGAA	2280
QY	2413	ACACCAATTCCTCTTCACAGACACTACGTGGGGCCCAAAATGGGCTTTAAAAGTCTGGCTC	2472
Db	2281	ACACTAAATTCCTGCTCTCAACCACTACGTGGGGCCCAAAATGGGCTTTAAAAGTCTGCTC	2340
QY	2473	AGGAGGCCACAGATTGGCAGACAGCCATGTTTCAAGTCAAGCCAGTAACTGAGCAACTGG	2532

Db	2341	AGGAGGCCACAGATTAGCAGAAAGCCAGTTGATGACGACAGTAACTGAGCAACTGA	2400
OY	2533	CAAGAGAAACCAGAGATATTCCAAAGAGCTGATGTCAGTGCAGGAGCTCTGAGG	2592
Db	2401	CAAGGAAACAGAGACTATTCCAAACAGCCCTCTCAGCTGTCGCAAGGCCCTGCATG	2460
OY	2593	AAGGAG-----GCGGAAGCGGGAGCCTGGAAGGAGCGGCTGTGTCAAAGGCTTGTGGAA	2646
Db	2461	AAGGAGTCGGAAGGCGGAGCGGTAGCCCGAGCGGTGCTGTGTGTCAGAGGGCTTGTGAAA	2520
OY	2647	AATTGCAGAAAACCTAAATCTCTGCCCCAGAGATTGTGAGAGGAGGCCACGCAACGACA	2706
Db	2521	AATTGGAGAAAACCAAGTCCCTGGCCAGCAGTGTGACAAAGGAGGCCACTCAAGCGAAA	2580
OY	2707	TGGAAGCAGATAGGCTTTATCAGATATGTGTCACCTTCATCAATTCGCTGTCAATTC	2766
Db	2581	TTGAAGCAGATAGGCTTTATCAGCAGACAGCTCTCCGCTCTGTGATTCAGTGTCTCGGCTTC	2640
OY	2767	AGGAGATCAATGATCAGTCTCTTGCAGGT--AGAAAGCAGAGAGGCTCAGACAAAAAGCTG	2823
Db	2641	AGGAGATCAGTATGATCAGTCTCTTCAAGGTGGAAGAAGCAAAAGAGGATCAACAAAAACGG	2700
OY	2824	ATTCTCTCTCAACCGTGTGACTTACATATGATGTGATGTTCAAGCAGTGCATAAGCATC	2883
Db	2701	ATTCACTCTCAAGCCTGGTATCCAGGCAATGTGATGTGATTCACACGTCACAGAAATATC	2760
OY	2884	TGGGAAATCGGGAAGAAAGAAACCCGGGAGCTCTTACAGAAATGSAADAATATGGGAGACGA	2943
Db	2761	TGGAAACTGGAAGAAAGAAAGAACACAGCAGCTTTCACAGAAATGSAADAATGGAAGACGA	2820
OY	2944	CATCAGATCAGCTCTTCCCGTCCCAACCTTGTCTAAAGAGCAGAGCCCAAGAACACTTAA	3003
Db	2821	AATCAGATCAGCTCTTCCCGTCCCAATCTTGTCTAAAGAGCAGACAAAGAACACTGA	2880
OY	3004	GTATGGGCAATGCCACTTTTATGAAAGTTGGAACATCTTAAAGAACTCAGAGATTG	3063
Db	2881	GTATGGGCAATGCCACTTTTATGAAAGTTGAGACATCTTAAAAACCTCAGAAAGTTTG	2940
OY	3064	ACCTGACAGGTTGAGATTTAAAGACAGAGAGCTGAAGAGGCCCATGAAGATCTCTCCACA	3123
Db	2941	ACCTGACAGTGGACACACAGAAABACAGAGGTGAAGAGGCCATGAAGATCTCTCCACA	3000
OY	3124	TCACCCAGAAAGGTTGACAGGTGCCAGTGCACAGACGAAGCAAGCAAGACAGCCCTGGGCA	3183
Db	3001	TCACCCAGAAAGGTTTCAAGATGCCAGTGCACAGACCCAGCAAGCAAGAAAGCCCTGGGGA	3060
OY	3184	GTGCTGCTGCCGAGCCCGACAGAGGCCAAAGAAATGCAGCCAGGAGGCCCTGGAGATCTCTG	3243
Db	3061	GCCTGTGCTGCATGATGCACAGAGGGCAAAAGAAATGGGGCGGGAGGCCCTGGAAATCTCCA	3120
OY	3244	GCAAGATTTGAACAGAGAGATAGGAGGTGCAACTTGGAAAGCCCAATGTACACAGCAATGAG	3303
Db	3121	GTGAGATTTGAACAGAGAGATAGGAGGTGCAACTTGGAAAGCCCAATGTACACAGCAATGAG	3180
OY	3304	CCTTGCCCATGAGAAAGGAGTGGCCACTCTGAAAGAGTGAAGATAGAGAAAGTGAAGAG	3363
Db	3181	CCTTGCCCATGAGAAAGGAGTGGCCCTCTCGAAGAGTGAAGATAGAGAAAGTGAAGAG	3240
OY	3364	AGCTGTCAAGAGAGAGCAGGATTTGACATGATATGACGACGACAGTGCAGATGTAATTG	3423
Db	3241	AGCTGTGAAGAGAGAGCTGAGATTTGACAGAAATATGAGATGACAGTACAGATGCTGATTA	3300
OY	3424	CAGAGGCCCAAGAGGTTGAAAACAGAGCCAAAGAAATGTGAGGATTAACATCCAAACACAC	3483
Db	3301	CAGAGGCCCAAGAGGTTGATACCAAGAGCCAAAGAGCTGGGGTTTACATCCAAACACAC	3360
OY	3484	TCAACACATTTGATGATGATCTCTTACACCTTAATATAGACACAGCCCTGAGTGTGATGAAGA	3543
Db	3361	TCAACACATTTAGAGGGCTCTCTGCATGTGATGAGACAGCCCTCTCAGTGTATGATGAAGG	3420
OY	3544	GGCTGATCTTACTGGAGCAGAGGCTTTTCCGAGCCCAAGACTTCAGATCAACAGCCAGCTAC	3603

Db	Query Match	Best Local Similarity	Matches 3318; Conservative	Score 73.9%;	DB 12;	Length 5460;
Db	3421	GGCTGGTCTTACTGGAGGACGAGAGCTTTCCGAGCCCAAGACCCAGATCAACAGCCACTGC	3480			
Qy	3604	GGCCCTTGATGTCAGAGCTGGAAGAGAGGGACATGGCAGAAAGGGCCACCTCCGTTTC	3663			
Db	3481	GGCCCATGATGTCAGAGCTGGAAGAGAGGGCACGCTAGCAGAGAGGGCCACCTCATTTGC	3540			
Qy	3664	TGGAGATGACATAGATAGTGGGATTCTGGCTGATGTGAAGAACTGGAGACATCAGGGACA	3723			
Db	3541	TGGAGACAAGCATAGATAGTGGGATTCTGGCTGATGTGAAGAACTGGAGACATTTAGGGACA	3600			
Qy	3724	ACCTGCCCCGGGCTCTCAATACCAGGCTTTGAGCAACGTGAAGTGGCTTTAGAG	3783			
Db	3601	ACCTGCCCCAGGCTCTCAATACCAGGCTTTGAGCAACGTGAAGTGGCTTTAGAG	3660			
Qy	3784	ATTTCACCAAGAGTTCTTGAGATTCAGACCTAGCTTGAAGATTTCTCA	3837			
Db	3661	ATTTCACCAAGAGTTCTTGAGATTCAGACCTAGCTTGAAGATTTCTCA	3714			
RESULT 8						
US-10-044-090-558						
Sequence 558, Application US/10044090						
Patent No. US20020137081A1						
GENERAL INFORMATION:						
APPLICANT: Olga Bandman						
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION:						
FILE REFERENCE: PA-0028 US						
CURRENT APPLICATION NUMBER: US/10/044, 090						
CURRENT FILING DATE: 2002-01-09						
NUMBER OF SEQ ID NOS: 850						
SOFTWARE: PERL Program						
SEQ ID NO 558						
LENGTH: 5460						
TYPE: DNA						
ORGANISM: Homo sapiens						
FEATURE:						
NAME/KEY: misc_feature						
OTHER INFORMATION: Incyte ID No. US20020137081A1 149791.5						
US-10-044-090-558						

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Db 432 ACCAGGTTGACAGGAGCCGATGGGACGATGTCTGGCCAGCTTCCACATGCTCAGC 491  
QY 570 GATGTGGGTGCGCCCAAGACCAAGAGCTGCTAGACTCCAAAGTGTGACTGTGACCCAGCT 629  
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Db 492 GATGGGGGTGACCCCAAGACCAAGAGACTCTAGACTCCAAAGTGTGACTGTGACCCAGCT 551  
QY 630 GGCATCTCAGGGCCCTGTGTGACTCAGGCCGCTGTGTGTGCAAGCCGGCTGTCACTGTGAGAG 689  
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Db 552 GGCATGTGCAAGGGCCCTGTGTGAGCGGGCCGCTGTGTGTGCAAGCCAGCTGTCTACTGTGAGAA 611  
QY 690 CGGTGTATGATGTGTGACACAGGTCTATCATCTGGATGGGGGAAACCCCTGAGGGCTGT 749  
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Db 612 CGGTGTATGATGTGTGATCAGATAGGTTACTATATCTGGATGGGGGAAACCCCTGAGGGCTGT 671  
QY 750 ACCAGTGTGTTTGTCTATGGGCAATTCGCGAGCTGCGACAGCTCTGGGGAGTCAAGTGTG 809  
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Db 672 ACCAGTGTGTTTGTCTATGGGCAATTCAGCCAGCTGCGCGAGCTCTGTGAGAAATACAGTGTG 731  
QY 810 CATAAATCATCTCTGCTCTCCATCAAGATGTTGATGGCTGGAAAGCTGTCCAAAGAAC 869  
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Db 732 CATAAATCATCTCTGCTCTCCATCAAGATGTTGATGGCTGGAAAGCTGTCCAAAGAAC 791  
QY 870 GGGTCTCTGCAAGGCTCCAGTGTGACAGCGCCATCGGGATATATTTACTCAGACGA 929  
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Db 792 GGGTCTCTGCAAGGCTCCAGTGTGACAGCGCCATCGGGATATATTTACTCAGACGA 851  
QY 930 CGATCAGACCCCTGTCTATTTTGTAGCTCTGCGCAAAATTTCTGGGAATCAAGAGTGTAGC 989  
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Db 852 CGATGTAGACCCCTGTCTATTTTGTGGCTCTGCGCAAAATTTCTGGGAATCAAGAGTGTAGC 911  
QY 990 TACGGGCAAGCTTATCTTTTGTAGCTACACGCTGTGGATGAGGGAGCGACACCCATCTGCC 1049  
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Db 912 TATGGTCAAGAGCTGTCTGTGACTACCGTGTGACAGAGAGGAGCCACCATCTGCC 971  
QY 1050 CATGAGTGTATCTCTGGAAGGTGTGTGCTATACGAGTACAGCTCCCTGTGATGCCACTTACG 1109  
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Db 972 CATGATGTATTTTGTGAAGGTGTGTGTGCTAGGATCAGCTCCCTGTGATGCCACTTGTGC 1031  
QY 1110 AAGACATGCTCTGTGGGATCACCAGACTTACACATTCAGATTAATGAAATGCCAAGC 1169  
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Db 1032 AAGACATGCTCTGTGGGATCACCAGACTTACACATTCAGATTAATGAAATGCCAAGC 1091  
QY 1170 AGTAAATGGAGCCCCAGCTAACTTACTTGTGATGTGAGGTTACTGCGGAACCTCACA 1229  
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Db 1092 AATAAATGGAGCCCCAGCTAACTTACTTGTGATGTGAGGTTACTGCGGAATCTCACA 1151  
QY 1230 GCCCTGCGGATCCGAGTACTACGGAGAAATACAGTACGTGGTACATGTCACAGTGTGACC 1289  
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Db 1152 GCCCTGCGGATCCGAGTACTACGTAAATACAGTACGTGGTACATGTCACAGTGTGACC 1211  
QY 1290 TTGATTTCAAGCCCGCCGCTTCTGTGAGCCCCAGCCGCTGGTTGAACATGTGTATGC 1349  
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Db 1212 CTGATTTCAAGCCCGCCGCTTCTGTGAGCCCCAGCCGCTGGTTGAACATGTGTATGC 1271  
QY 1350 CCTGTGGGTCAAGAGGGCAGTTCTGCGAGATTTGTGCTTCCGGCTACAAAGAGATTCA 1409  
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Db 1272 CCTGTGGGTCAAGAGGGCAGTTCTGCGAGATTTGTGCTTCCGGCTACAAAGAGATTCA 1331  
QY 1410 GCCAGACTGGGACTTTTGGCACCTGTATTCATGTAACTGCCAAGGGGAGGGGCGCTGC 1469  
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Db 1332 GCGAGACTGGGACTTTTGGCACCTGTATTCATGTAACTGCCAAGGGGAGGGGCGCTGC 1391  
QY 1470 GATCCAGACAGAGACTGTTACTCAGGGGATGAGAACCTTCACATCTCCGTGATGTGCT 1529  
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Db 1392 GATCCAGACAGAGACTGTTACTCAGGGGATGAGAACATCTGATCACT---TGAGTGTGCT 1448  
QY 1530 GACTGCCCATTTGTTTCTACAAAGATCCAAAGACCCCGGAGCTGTCAAGCCGTGCC 1589  
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Db 1449 GACTGCCCATTTGTTTCTACAAAGATCCGACAGACCCCGGAGCTGTCAAGCCATGTGCC 1508  
QY 1590 TGTCCGAATGGGTGAGCTGCTCCGTGATGCCAGACAGAGAGGTGTGTGCAATTAAC 1649  
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Db 1509 TGTCAATACGGGTTCAAGCTGCTCACTGATGATCCGAGACGAGAGAGGTGTGTCAATTAAC 1568  
QY 1650 TGCCTCCAGAGGTGTCACTGTGTGCTGCTGAGCTCTGTGCTGATGGCTATTTTGGGGAC 1709  
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Db 1569 TGCCTCCAGAGGTGTCACTGTGTGCTGCTGAGCTCTGTGCTGATGGCTATTTTGGGGAC 1628  
QY 1710 CCTTTCGGGGAGCTGTGGCCAGTGTAGGCTTGTGACGCTTGTGACGCTGTGACAAACAAGTGTG 1769  
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Db 1629 CCTTTCGGGGAGCTGTGGCCAGTGTAGGCTTGTGACGCTTGTGACGCTGTGACAAACAAGTGTG 1688  
QY 1770 GACCTAGTGTGCTGCGGGAACTGTGACGCTGTGACGCTGTGACGCTGTGACGCTGTGACGCTGTG 1829  
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Db 1689 GACCTAGTGTGCTGCGGGAACTGTGACGCTGTGACGCTGTGACGCTGTGACGCTGTGACGCTGTG 1748  
QY 1830 AATCAGCTGGGGTCCACTGTGTGACAGTGTGACAGAGCTTACTATGTGGGACCCGTTGGCT 1889  
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Db 1749 AATCAGCTGGGGTCCACTGTGTGACAGTGTGACAGAGCTTACTATGTGGGACCCGTTGGCT 1808  
QY 1890 CCTAATTCAGACACAAAGTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTG 1949  
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Db 1809 CCTAATTCAGACACAAAGTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTG 1868  
QY 1950 GAGTGTGAAAGTGTGAGTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTG 2009  
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Db 1869 GAGTGTGAAAGTGTGAGTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTGACGCTTGTG 1928  
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8      : APPLICANT: Tiyygvason, Karl
9      :           kalliunki, Pekka
10     :           Pyke, Charles
11     : TITLE OF INVENTION: Laminin Chains: Diagnostic Uses
12     :
13     : NUMBER OF SEQUENCES: 20
14     :
15     : CORRESPONDENCE ADDRESS:
16     : ADDRESSSEE: Fay Sharpe Fagan Minnich & McKee
17     : STREET: 1100 Superior Ave, Suite 700
18     : CITY: Cleveland
19     : STATE: Ohio
20     : COUNTRY: USA
21     : ZIP: 44114
22     :
23     : COMPUTER READABLE FORM:
24     : MEDIUM TYPE: Floppy disk
25     : COMPUTER: IBM PC compatible
26     : OPERATING SYSTEM: PC-DOS/MS-DOS
27     : SOFTWARE: PatentIn Release #1.0, Version #1.30
28     :
29     : CURRENT APPLICATION DATA:
30     : APPLICATION NUMBER: US/09/756,071B
31     : FILING DATE: 08-Jan-2001
32     : CLASSIFICATION: <Unknown>
33     :
34     : PRIOR APPLICATION DATA:
35     : APPLICATION NUMBER: US 09/663,147
36     : FILING DATE: 150-September 2000
37     :
38     : ATTORNEY/AGENT INFORMATION:
39     : NAME: Minnich, Richard, J
40     : REGISTRATION NUMBER: 24,175
41     : REESENTATION/DOCKET NUMBER: TRV 20014
42     : TELECOMMUNICATION INFORMATION:
43     : TELEPHONE: 216-861-5582
44     : TELEFAX: 216-241-1666
45     :
46     : INFORMATION FOR SEQ ID NO: 14:
47     : SEQUENCE CHARACTERISTICS:
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51     : TOPOLOGY: linear
52     : MOLECULE TYPE: cDNA
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68     : FEATURE:
69     : NAME/KEY: polyA_site
70     : LOCATION: 4296
71     :
72     : SEQUENCE DESCRIPTION: SEQ ID NO: 14:
73     : US-09-756-071B-14

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14	AAGAAAAAGAAAGCAGACAGCGAGGAGGAGAGATGAGAACACCAAC--CGAGCGCGGAGC	71		
159	AGCGACCCCTGCAAGCGCG-----GACCGCGCGCGGCGCTGGCCATGCTGCGCTGTG	211		
72	AGCGACCCCTGCGAGCGGAGACAGAGACTGAGGGGGCGGACCGCCATGCGTGGCGCTGTG	131		
212	GCTGAGCTGCTACCTCTGCT	271		
132	GCTGGGCTGCTGCT	191		
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132	GGAATCTGTATTTCAATGGAATCCAGGCAATGCAATCTTTGACAGAGAACTTCACAA	251		
332	ACAGACAGAAATGATTCGCGCTGCTCACTGCAATGACAACTGATGGCATCCACTG	391		
252	ACAACTGTATGATTCGCGCTGCTCACTGCAATGACAACTGATGGCATTCCTG	311		
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372	TTGTATCTTAAAGTTCTTAGGCGCTGATGATGATCAACTGTGAGGAGGAGGAGGAGG	431		
512	GCCAGGTTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	571		
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Qy	1172	TAATTGGAGCCCCAGCTAAGTTACTTGTAGTATCGAGGTTACTGGGAACTCAGAGC	1231
Db	1092	TAATTGGAGCCCCAGCTGAGTTACTTGTAGTATCGAGGTTACTGGGAACTCAGAGC	1151
Qy	1232	CCTGGGGATCCGAGCTACTACGGAGATATAGTACGTGGGTACATTCAGACGTCATT	1291
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Qy	1292	GATTTTCACGCCGCCCTGTTCCTGTGAGCCCCAGGCCCTGGGTTAAACATGTGATGCC	1351
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Qy	1352	TGTTGGCTACAAAGGGGCAATTCTGCAGAGATTGTGCTTCGGGCTACAAAGATTTAGC	1411
Db	1272	TGTTGGGTACAAAGGGGCAATTCTGCAGAGATTGTGCTTCGGCTACAAAGAAATTTAGC	1331
Qy	1412	CAGACTGGGACCTTTTGGACCTGTATTCATCTGTAACTCGCCAAGGGGAGGGGCTCGA	1471
Db	1332	GAGACTGGGGGCTTTTGGACCTGTATTCCTTTACTGTACAAAGGGGAGGGGCTCTGA	1391
Qy	1472	TCACAGACAGAGAGATGTTACTCAGGGGATGAGAACCTTGACATCCCTGAGTGTGTA	1531
Db	1392	TCACAGACAGAGAGATGTTATTTCAAGGGGATGAGAAATCCTTACAT---TGAGTGTGCTGA	1448
Qy	1532	CTGCCCCATTTGGTTTCTACAAAGATTCACAGACCCCCGGAGCTGCMAAGCCGTGCCCTG	1591
Db	1449	CTGCCAATTTGGTTTCTACAAAGATTCGCACAGACCCCCGGAGCTGCMAAGCCATTCCTGTG	1508
Qy	1592	TCGCATATGGGTTTCAGCTGCTCCGTATGCCCTGAGACAGAGAGAGGTGTGTGCATTAAGT	1651
Db	1509	TCATTAACGGGTTTCAGCTGCTCAGTGATTTCCGGAACAGGAGAGGTGTGTGCATTAAGT	1568
Qy	1652	CCCCAGGGTTCACGTGTGCCGCCCTGTGAGACTCTGTGTCTGATATGGGCTATTTTGGGGACC	1711
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Db	1629	CTTGTGTGAACATGTGCCAGTAGGAGGCCCTTGTACAGCCCTGTCTAATGAACAACATGTGA	1688
Qy	1772	CCCTAGTCCCTCCGGGAACCTGTGACCGCCTACACAGCAGGTGTGTGAATGTATCCACA	1831
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: APPLICANT: Tiyyavasan, Karl
: APPLICANT: Doi, Masayuki
: APPLICANT: Thyboll, Jill
: TITLE OF INVENTION: Recombinant Laminin 10
: FILE REFERENCE: 99-274-F
: CURRENT APPLICATION NUMBER: US/10/037,182
: PENDING FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 60/257,449
: PRIOR FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/279,282
: PRIOR FILING DATE: 2001-03-28
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: ORGANISM: Homo sapiens
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: NAME/KEY: CDS
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US-10-037-182-15

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QY	938	CCCCTGTCAATTTTGTAGTCTCTGCCAAATTTCTTGGGATATCAACAGTGTACGGGCA	997
Db	1566	TCCCTCGTACTCAATGTCTCTCGCAAAATTTTGGCGCAAGCAGGTGTGAGTATGTGCA	1625
QY	998	AAGCTATCTTTTGACATCCATCGCTGTGGATGAGGGAGGCGAGACACCATGTGCCATGAGCT	1057
Db	1626	GAACCTCTCCCTTTCCTTTTCGATGTGAGAGCGGCAAGATATCTGCCCTCTGTGCCAAGACT	1685
QY	1058	GATCCTGGAAAGTCTGTGTCTACAGGATCACAGCTCCCTTGATGGCATTACCAAGACACT	1117
Db	1686	TGTGCTTGAGGAGACTGGCTTAAAGATATGTACCTTGATTCGCTGAGGCAATTCCTTA	1745
QY	1118	GCTTGTGGGATCACCAAGACTTTCACATTTAGATTAAATGAATCCACAGACTAATTG	1177
Db	1746	TCCAAGTGAACCACTGTGAATATGTCTTAGGCTCCATGAAGCAACAGATTACCCCTTG	1805
QY	1178	GAGCCCCAGCTAATGTTACTTGTGATCGGAGGTATCTGGGAAACCTCACAAGCCCTGCG	1237
Db	1806	GAGGCTGTCTTACCCCTTTTGATTTACAGAGCTCCTAAACAATTGACTCTATCAAA	1865
QY	1238	GATCCGAGCTACTACGAGGAATACAGTACTGGGTACTATGACAACGTCGACTTGATTTTC	1297
Db	1866	GATACGTGGGACATACAGTGAAGAGAGTGCGATATTGGATGATGTACACCTGGCAG	1925
QY	1298	AGCCCCGCTTTTCTGTGAGCCCCACGCGCCCTGGGTGTAACAATGTGTATCCCTGTGG	1357
Db	1926	TGCTGTCTGTGGGCTGTGAGTCCCTGTCAACTTGGGTGTGAGTCTGCACCTCTCTGTGGG	1985
QY	1358	CTTACAAAGGAGATTGCCGCCAGGAATGTGCGTCCGGGCTACAAAAGATTCAGCAGACT	1417
Db	1986	ATATGAGAGGCGAGTTTGTGTGAGATGTGCTCTCAAGTTTACGAAGAAGAACTCTTAATCT	2045
QY	1418	GGGACCTTTTGGCACTGTATTTCCATGTATTCATGCGCAAG--GGAGGGGCGCTCGATCC	1474
Db	2046	TGACACATACGTCCATGTGTGTGCTTTGGCGCTGCATATGGAACAGCAGAGACTGTGATCC	2105
QY	1475	AGACACAGGAGACTGTATCTCAGGGATGAGAACCTTGACATCCCTGATGTGCTGACTG	1534
Db	2106	TGAACACAGGTGTGTGTAACTCCAGAAGCAATAACGGCTG---GCCGCACTGTGAAAGTGT	2162
QY	1535	CCCCATGTTGTTTACAAACGATTCACAAGA-----CCCCCGCAGCTGCAAGCCGTGCC	1588
Db	2163	CAGTGAATGGGTACTATGAGAAATTCACATGCAAGGACCTCCCTCGAATGCCAAACCTGTCC	2222
QY	1589	CTGTCCGAATGGGTTACAGCTGCTCCGTGATGCTGTAGACACAGAGAGGTGGGTGCATATA	1648
Db	2223	GTGTCTGTGAGAGTTCAAGTTGTGTGTGTTTCCCAAGACAAAGAGGTGGTGTCAACCA	2282
QY	1649	CTGCCCCAGGGTGTACGTGTGCCGTGTGAGCTCTGTGCTATGAGGTATTTTGGGGA	1708
Db	2283	CTGTGCTACGTGCACCACTGTTAGAGATGTGAGACTCTGTGTATGTATGCTACTTTGGAGA	2342
QY	1709	CCCCCTTGGGGACGTGGCCCACTGAGGCGCTTGTACGCCCTGTGATGTGCAACCAACGT	1768

Db	2343	CCCCCTGGGTAGAAACGGCCCTGTGAGACTTTGGCCGCTGTGCCAGTGCATGACAAACAT	2402
OY	1769	GGACCCTAGTCCCTCCCGGAACTGTGACCGCCTTGACAGCAGGTGTGAAAGTCATCA	1828
Db	2403	CGATCCCAACCAAGTTGGAAATGTCAATCCGTTGACGGGAAGAAATCCGTAAGTGCACCTA	2462
OY	1829	CAACAAGCTGTGGGGCCACTGTGACCACTGCAAGCAAGCGGTACATGAGGGACCCGTTGCC	1888
Db	2463	TAAACATCTGTGGCTTCTAATTTGTGACCGGTGCAAAAGACGATTTTTTTGGAAATCCCTGGC	2522
OY	1889	TCCCAATCCAGCAGACAAGTGTCCAGCTTGCACTGCACCC 1930	
Db	2523	TCCCAATCCAGCAGACAAGTGTCAAAAGCCTGCAATTTGCAATCC 2564	
RESULT 12			
US-10-037-182-13			
US-10-037-182-13			
Sequence 13, Application US/10037182			
Publication No. US20030044899A1			
GENERAL INFORMATION:			
APPLICANT: Tytgavason, Karl			
APPLICANT: Doi, Masayuki			
APPLICANT: Thyboll, Jili			
TITLE OF INVENTION: Recombinant Lamnin 10			
FILE REFERENCE: 99-274-F			
CURRENT FILING DATE: 2001-12-21			
PRIOR APPLICATION NUMBER: US/10/037,182			
PRIOR FILING DATE: 2000-12-21			
PRIOR APPLICATION NUMBER: 60/257,449			
PRIOR FILING DATE: 2000-12-21			
PRIOR FILING DATE: 2001-03-28			
NUMBER OF SEQ ID NOS: 36			
SOFTWARE: PatentIn Ver. 2.0			
SEQ ID NO 13			
LENGTH: 5306			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (260)..(5086)			
NAME/KEY: sig_peptide			
LOCATION: (260)..(358)			
US-10-037-182-13			
Query Match 12.9%: Score 515.6; DB 9; Length 5306;			
Best Local Similarity 58.8%: Pred. No. 1.2e-153;			
Matches 978; Conservative 0; Mismatches 654; Indels 30; Gaps 4;			
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Db	1282	CTGTGATTGCACATGGTGTGATCCCAAGGATGCTACTTGGACCCCTGAACCTCTATCTGTCCAC	1344
OY	338	AGGAAATGTGATTCGGCTGCTCACTGCAATGACAACAACATATATGGATCCACTGCGAGAG	397
Db	1342	TGGCCATGTGGGGCCACTGTATCAACTGCGAAGATPAACACAATATGGCGCCACTGTGAGAG	1401
OY	398	GTGCAAGCAGAGATTTTACCAGCAGACAGAGAAGAGGACCGCTGTTACCCTGCAATTTGTAA	457
Db	1402	GTGCCGAGAGACCTTCTTCGCCCTTTGGCAACAATGAAGCCGCTCTTCATGCCACTGTGAG	1461
OY	458	CTCTAAAGTTCTCTTACGCGTGTGATGTGACAACTGTGACGAGTGTGACGCTGTAAAGCAGG	517
Db	1462	TCTGTGTGGGCTCTCTTAAGACACAGCTGTGATGTAGTACGGGAGAGTGTAAAGCCAGG	1521
OY	518	TGTCAACAGAGACAGGTGTGACCGATGTCTGCCCCGCTTGACACACACTCACTGATGCTGG	577
Db	1522	AGTGATGTGGGGACAAATGTGTGACCGATGTGCCACCGATTCATTCCTCACTGAAGCAGG	1581
OY	578	GTGGGCCCAAGACCAAAAGGCTGTAGACTCCAACTGTGACGTGTGACCAAGCTGCATCTC	637
Db	1582	ATGCAAGGCCA-----TGCTCTTGTGTGATCCCTCTGCGACGATAGATGA	1623

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QY 638 AGGCCCTGTGATCAGGCCGCTGTCTGCAAGCCGGCTGTCTACTGTGAGAGCCGTGTGA 697
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1624 ATGTAATGTGTAAGCAGAGAAATGTGTTGCAAAAGCAATGTGCAAGCTTCAATTTGA 1683
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 638 TAGGTGTGACAGAGTTTACTATCAGCTGATGGGAAAACCTGAGGCTGTACCAATG 757
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1684 AAGATGCAAAACCTGGATTTTAACTGGAATCATATCTGCGGGTGTCCACCCCTG 1743
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 758 TTTTGTATGGGAGCTCCGCGAGCTGCGACAGCTGCGGGAGCTACAGTGCATTAAT 817
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1744 CTTCGCTTTGGGCAATTTCTTCTGTCTGTAACAACGCTTTGGCTACAGTGTATTAT 1803
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 818 CATCTCTCCCTTCATCAAGATGTGATGGCTGGAAGGCTGTCCAAGAAAAGGCTTCC 877
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1804 CTCTCTACCTTTGAGATGATGAGAGATGGGTGGCGGGAACAGAGATGGCTCGA 1863
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 878 TGCAAGCTCCAGTGTGACAGAGCCGAGTATATTAGCTACGACGACATCAGA 937
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1864 AGCATCTCTGAGTGTCTCTGAGAGGCAAGATATCCCGTATCTGACAGCTACTT 1923
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 938 CCCGTCTATTTTGTAGCTCCGCCAAATTTCTTGGGAATGACAGAGGTAGCTAGGGCA 997
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Db 1924 TCCTCGTACTTCACTTGTCTCCGCAAGTCTTGGGCAAGCGGTGTGAGTTATGTGA 1983
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 998 AAGCTATCTTTTGTACTACCGTGTGATAGGGAGGAGACACCATCTGCCATGACGT 1057
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Db 1984 GAACCTCTCTCTCTCTTTCAGTGTGACAGGAGGAGATATCTGCTCTGCGGAGACT 2043
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QY 1058 GATCTGGAAGTGTGTCTTACAGATCAGAGCTCCCTTGTATGCCATTTAGCAGACACT 1117
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Db 2044 TGTGTTGAGGAGGTGGCTTAAAGATCTGTACCTGTATCGCTGACGGCAATTTCTTA 2103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1118 GCTTGTGGGATCAACCAATTTACATTCAGATTAATGAACATTCACAGAGATTAAT 1177
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Db 2104 TCCAAATGACAGCACTGTGAAGTATGTCTTCAAGCTCCATGAGCAACAGATTAACCTTG 2163
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   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 1238 GATCCGACTACTTACGAGAAATACAGTACTGGGTACTTACAACTGACCTTATTTTC 1297
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Db 2224 GATACGTGGACATTCAGATGAGAGAGTGTGATTTGTGATGTGCACCCCTGGCAAG 2283
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QY 1298 AGCCCCGCTTTTCTGGAGCCCCAGCCGCTGGGTTAAACAATGTATGCTGTTGG 1357
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Db 2284 TGTCTGTCTGTGGGCTGGAGTCCCTGCAACTTGGGTGAGTCTCAGCTGTCTGTGG 2343
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1358 CTACAAGAGGAGTCTGCCAGATTTGTCTCCGCTACAAAGAGATTACGCCAGACT 1417
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2344 ATATGAGGGGAGTTTGTGAGATGTGCTCTCAAGTTACAGAGAGAGAACTCCTAATCT 2403
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QY 1418 GGGACCTTTTGGCACTTATTTCAATGTAAGTCCCAAG---GGAGGGGCTCTGGATCC 1474
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Db 2404 TGGACCAATACAGATGTGTCTTGGGCTTCATGTGACACAGCAGACCTGTGATCC 2463
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QY 1475 AGACAGAGAGACTTTTACTGAGGGGATGAGAAACCTGCATCCCTGATGTGAGACAG 1534
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2464 TGAGCAGAGTGTTTTAACTGAGAGACATTAAGGCTG---GCCGCACTGTGAGAAAGTG 2520
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Db 2521 CAGTATGGGTACTTGAAGATTTCAAGTCAAGCACTCCTCCGATTTGCAACCCGTGCC 2580
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QY 1589 CTGTGCAATGGGTCTAGCTGTCCGTGATGCTTACAGAGAGAGGTGTGTCAATTA 1648
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Db 2581 GTGTCTGTGAGGTTTAAAGTGTGTGTTTCCCAAGAACAAAGGAGGTGTGTGACCCAA 2640
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QY 1649 CTGCCCCAGGCTGCTACAGTGGGCCGCTGAGTGTGTGTGTGATTTTGGGGA 1708
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2641 CTGTCTACTGTGACACACTGTGTAAGAGATGTAGCTGTGTGATGATGGTACTTTGGAA 2700
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1709 CCCCCTTGGGGAAGCTGGGCCAGTGAAGGCTTGTCAAGCCCTGTGACACACAGACT 1768
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Db 2701 CCCCCGTGAGAAAGCGCCCTGTGAGACTTTGGCCGCTGTGCGAGTCAAGTGAACAT 2760
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QY 1769 GGAACCTAGTGCCTCCGGGAAGTGTGACCGCTGACAGAGGTGTGAGTGAATCCA 1828
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2761 CGATCCCAACGATTTGAAATTTGCAATTCGCTGACGGGAGAGAAATGCTGAAGTCACTA 2820
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1829 CAACACACTGTGGGTCACACTGTGACAGTGTGCAAGACAGCACTACTATGGGAGCCGTTGAGC 1888
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2821 TAACACTGTGCTTCTATTTGTGACCGGTTGCAAGACGATTTTGTGAATCCCTGCG 2880
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1889 TCCCAATCCAGACAGCAAGTGTGAGCTTGTGCAATGCAACCC 1930
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Db 2881 TCCCAATCCAGACAGCAATGCAAGCTGCAATTCGAATCC 2922
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RESULT 13
US-10-084-817-81
; Sequence 81, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO: 81
; LENGTH: 7812
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 252151.12
; NAME/KEY: unsure
; LOCATION: 3983
; OTHER INFORMATION: a, t, c, g, or other
US-10-084-817-81

Query Match      12.9%; Score 515.6; DB 9; Length 7812;
Best Local Similarity 58.8%; Pred. No. 1,6e-153;
Matches 978; Conservative 0; Mismatches 654; Indels 30; Gaps 4;

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Db 1724 AGATCAACACCTGGATTTTATATCTGCATCATTAATCTCGGGGTTGCAACCCCTG 1783  
 QY 758 TTTTGTCTAGGACATTCGCGCAGCTGCCACACAGCTCTGGGGACTACAGTGTCCATAAAT 817  
 Db 1784 CTTCGTCTTGGCATTCCTCTGTGTACAAACGGTGTGGGTACAGTGTATTTCTAT 1843  
 QY 818 CATCTGCTCTTCATCAAGATGTGTATGGCTGGAAAGCTGTCCAAAGAAAGGGGTCTCC 877  
 Db 1844 CTCCCTGACTCTCAATTTGATGAGATGGGTGGCGGCAACAGAGATGGCTCTGA 1903  
 QY 878 TGCAAAGCTTCAGTGGTCAAGGCGCATATATTAGTCTCAGCAGAGATCAGA 937  
 Db 1904 AGCATCTCTGAGTGTCTCTGAGAGGCAAGATATCCCGTGATCTCAGACGCTACTT 1963  
 QY 938 CCCGTCTATTATTGTAGTCTCTGCCAAATTTCTTGGGAATCAACAGGTAGCTACGGCA 997  
 Db 1964 TCTCGTGTACTTATGCTCTCTGCAAAAGTTCTTGGGCAAGCAGTGTGTATGTCA 2023  
 QY 998 AAGCCTATCTTTGACTACCGTGTGGATAGGGGAGCAGACACCATCTGCCATGACGT 1057  
 Db 2024 GAACCTCTCTCTCTCTCTGAGTGACAGGCGAGATACTCGCCCTCTGCGCAGACCT 2083  
 QY 1058 GATCCGSAAGGTGGTGTCTAGGATCAGCTCCCTTGATGCCACTTAGCAAGACT 1117  
 Db 2084 TGTGCTTGAGGGAGCTGGCTTAAGAGTATCTGACCTTGATCTCAGGGCAATTCCTA 2143  
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 Db 2144 TCCAAATGAGACACATGTGATATGTCTTCAAGGCTCCATGAAGCAACAGATTACCTTG 2203  
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 QY 1238 GATCCGAGCTACCTAGSAGAAATACAGTCTGGGTACATTGACAGTGAACCTGATTTG 1297  
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 QY 1298 AGCCCGCCCCGTTTCTGAGAGCCCGCAGCCCTGGTTGAACAATGTGTATGCCCTGTGG 1357  
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 Db 2801 GATCCCAACGAGTTGAAATGTGATGCTTGTGACGGGAGAAATGCTGTGATGATCTA 2860

QY 1829 CAACAGAGCTGGGGTCCACTGTGTGACCAAGTGCAGGAGGCTACTATGGGAGCCGTTGGC 1888  
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 Db 2921 TCCCAATCCAGACAGACAAATGCAAAAGCTGTGCAATTGCAATCC 2962

Search completed: July 6, 2003, 08:58:42  
 Job time : 608 secs